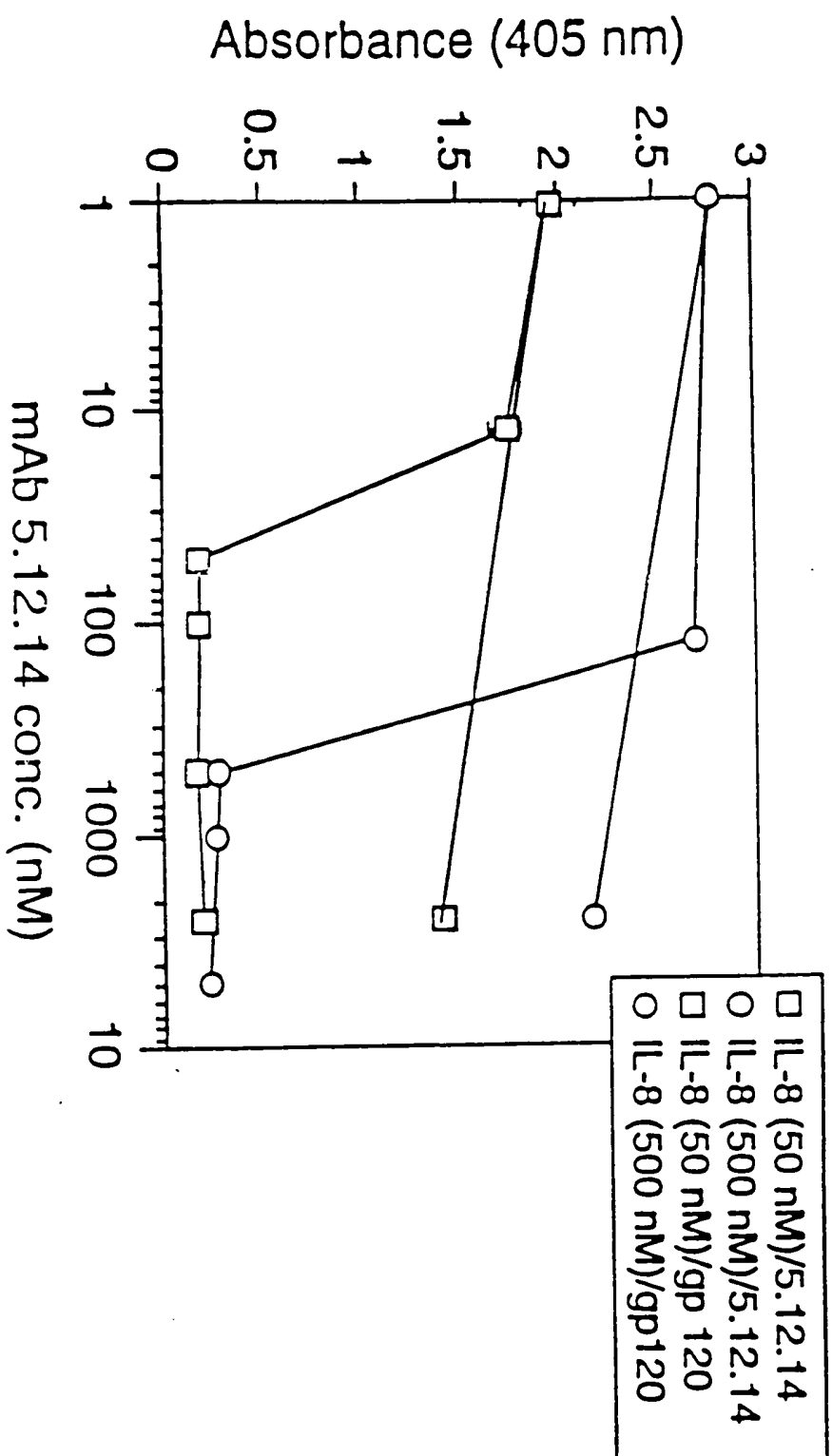
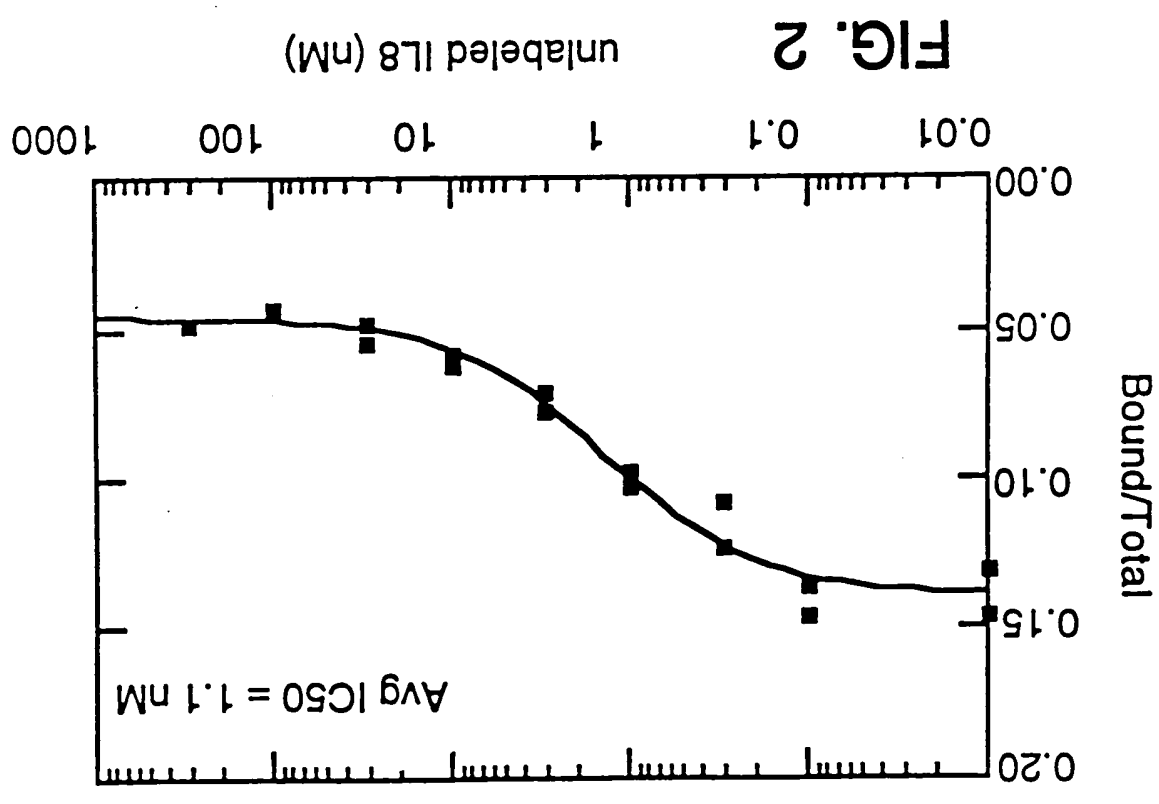
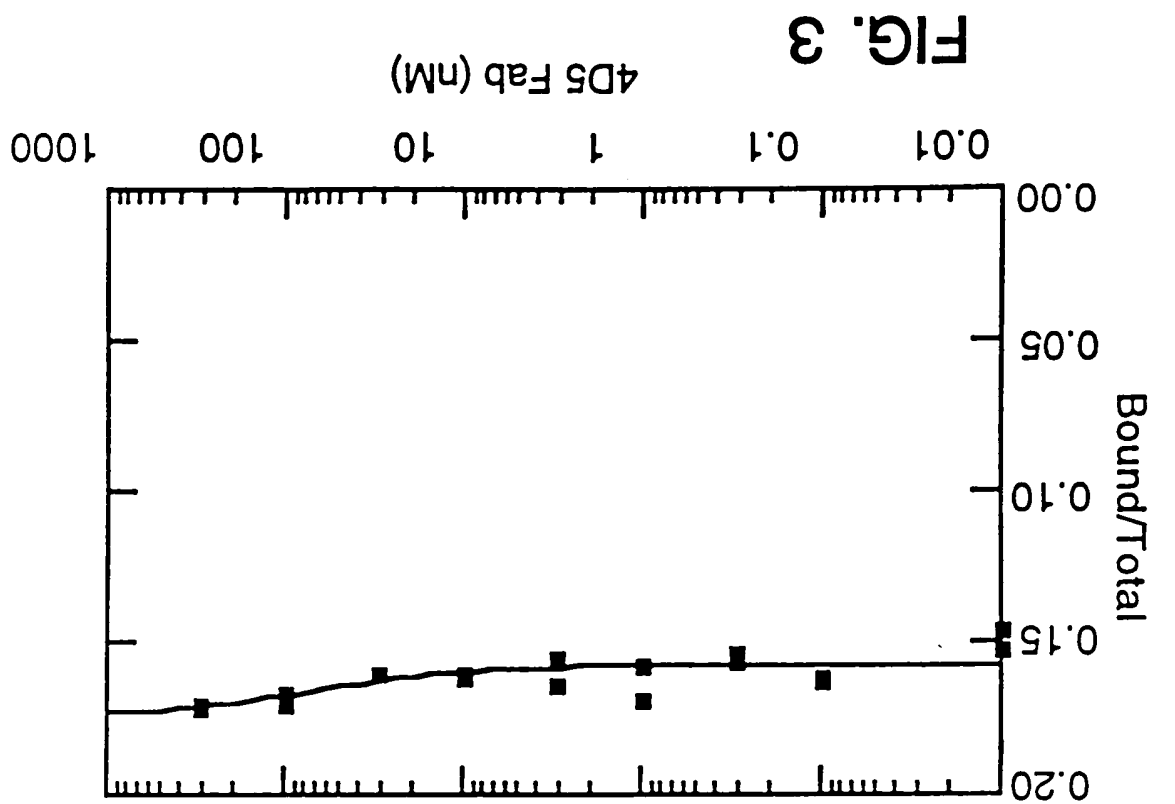


FIG. 1





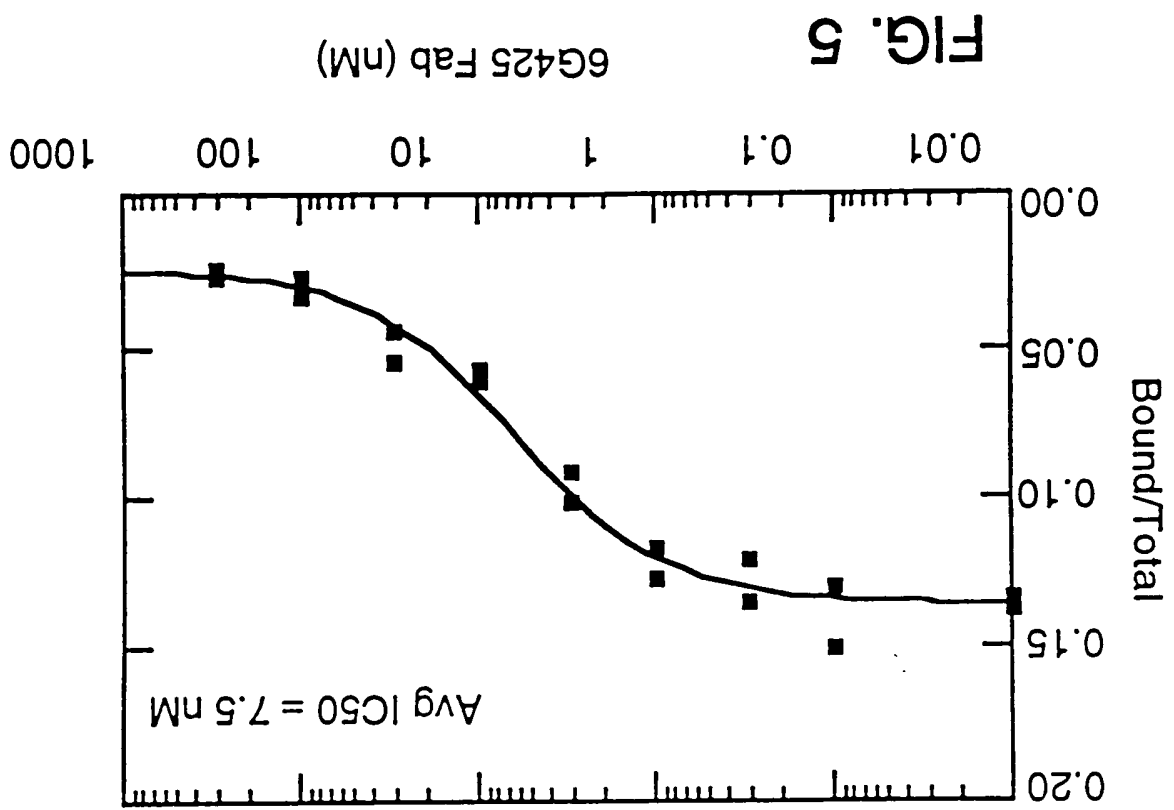
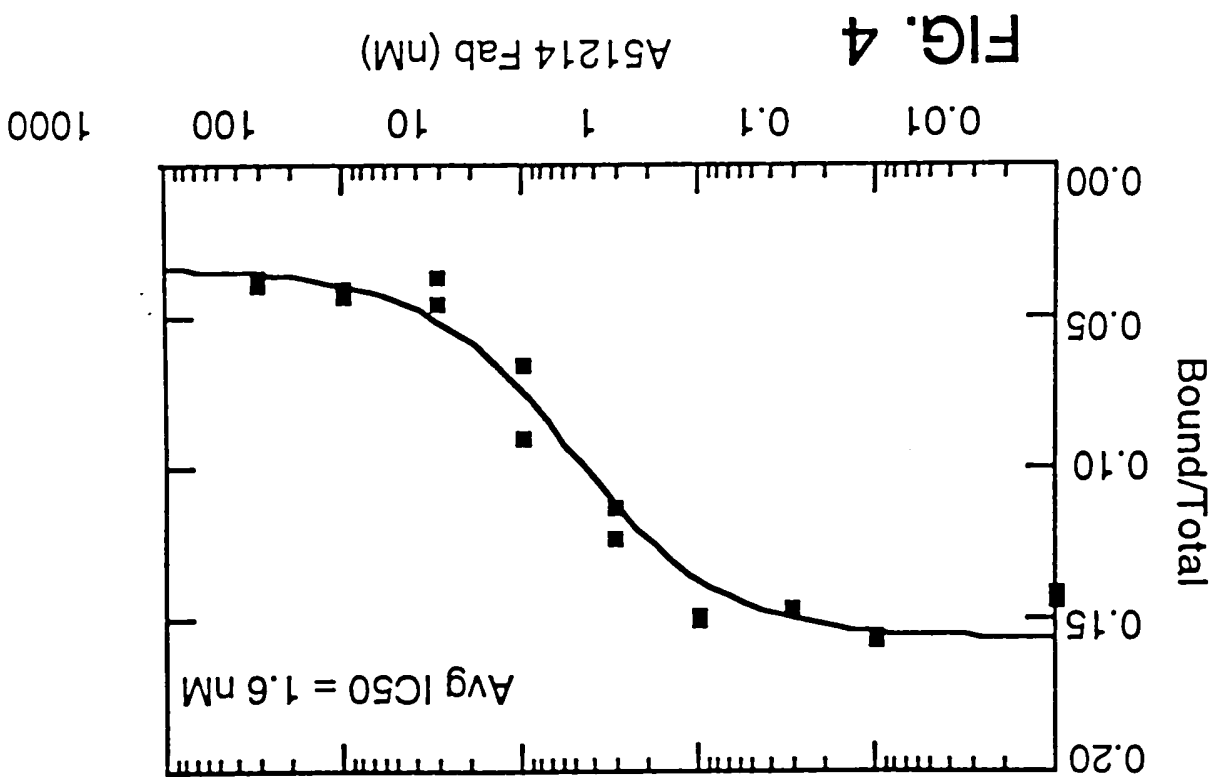


FIG. 6

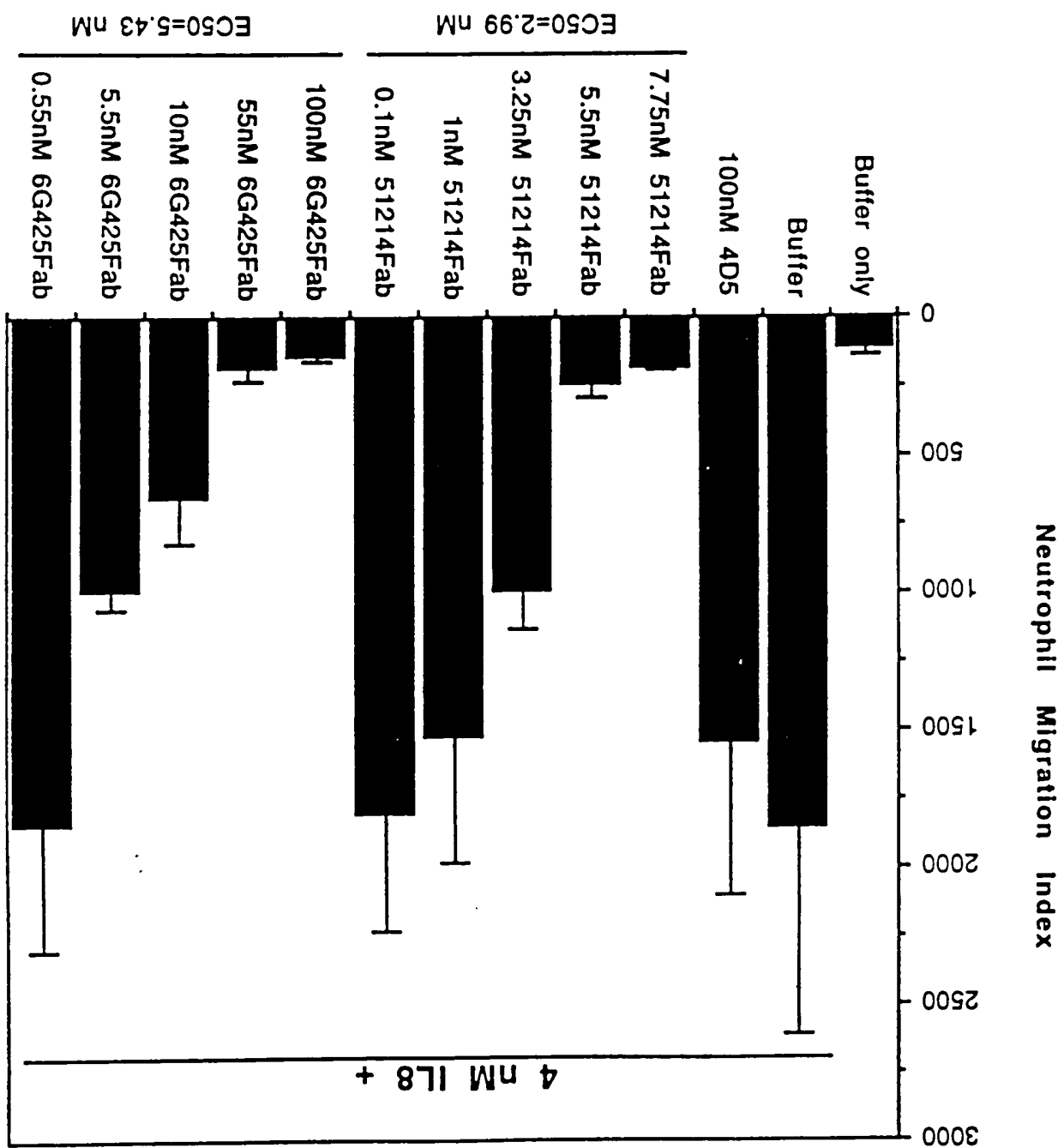


FIG. 7

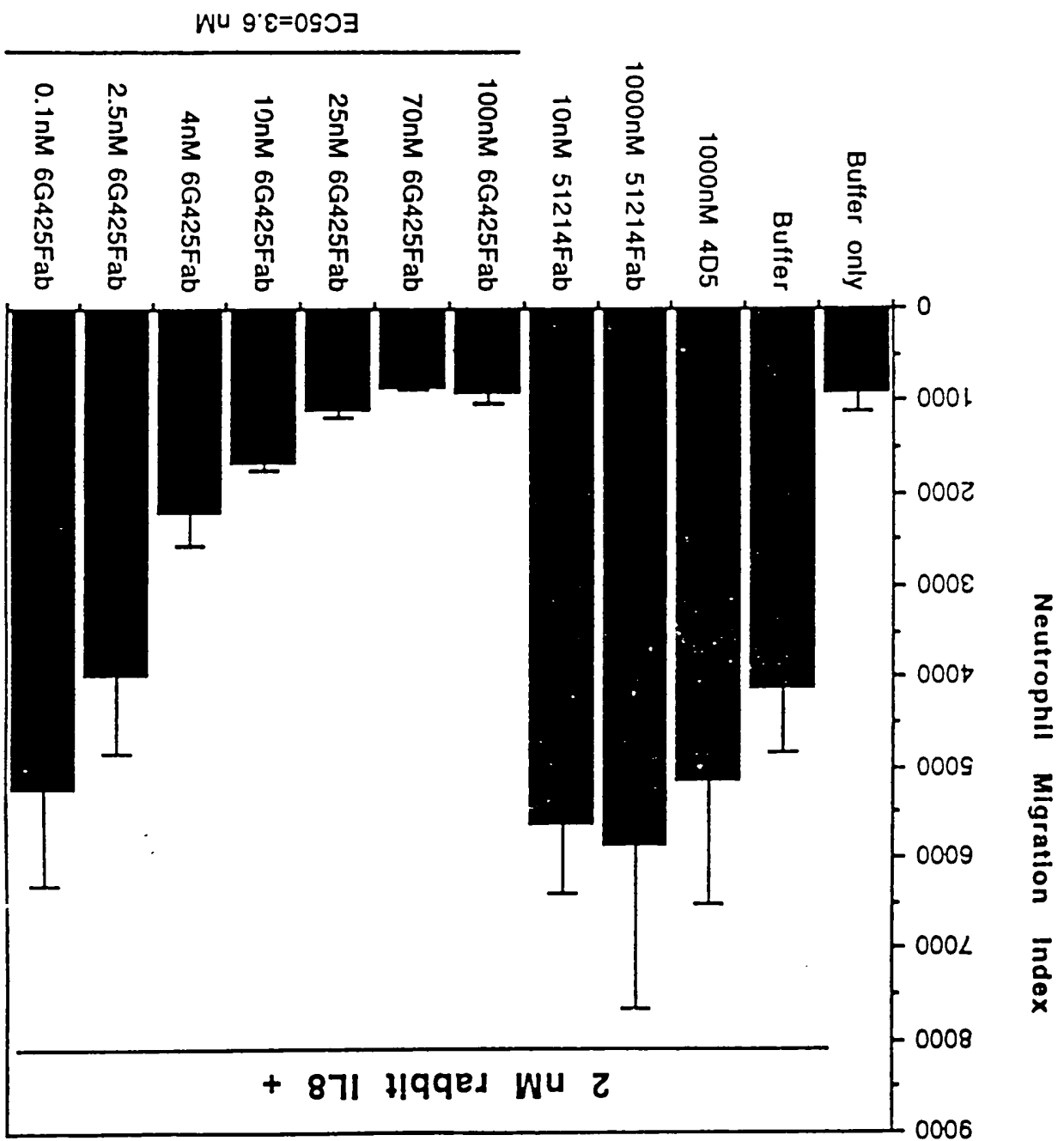


FIG. 8

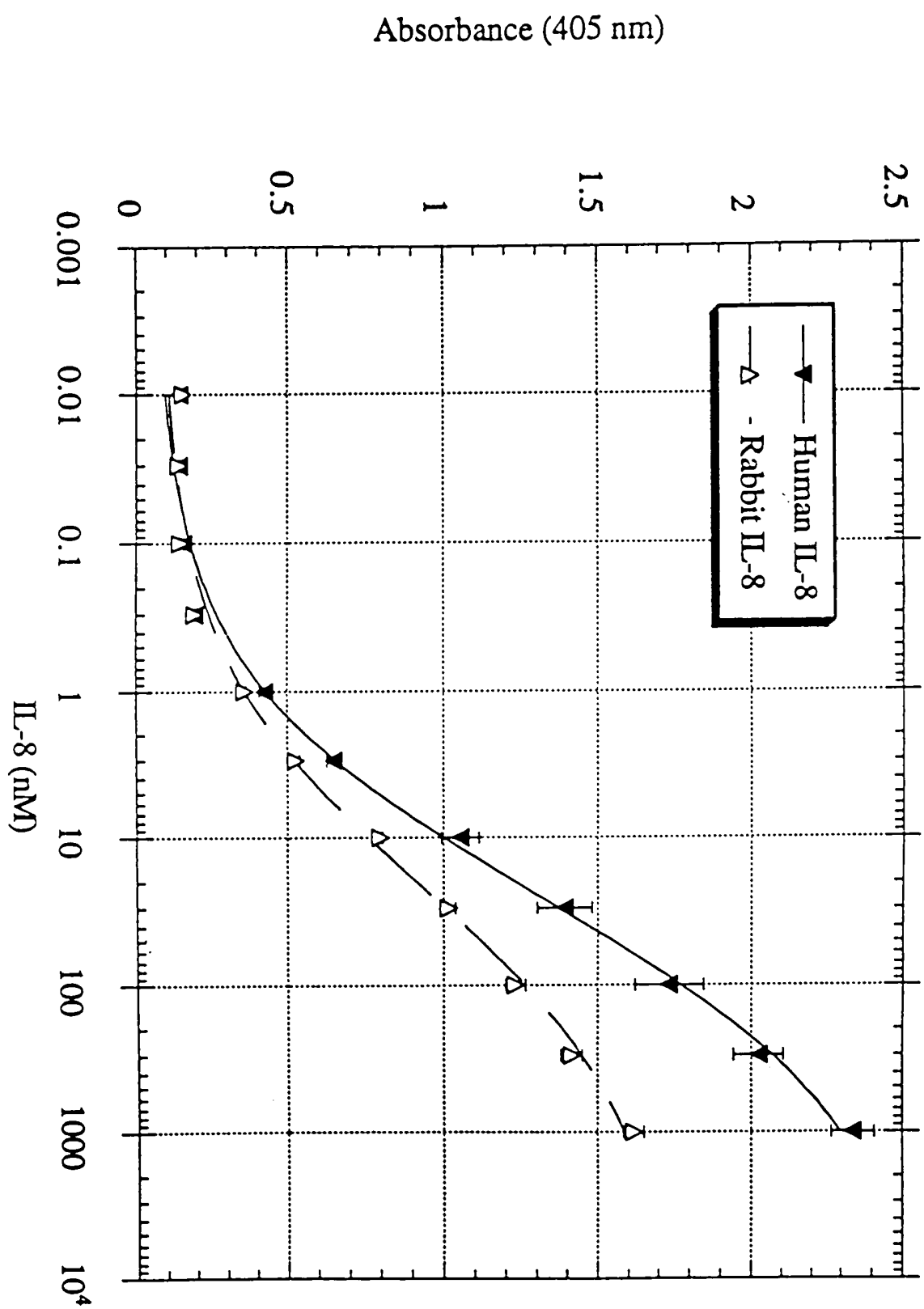


FIG. 9

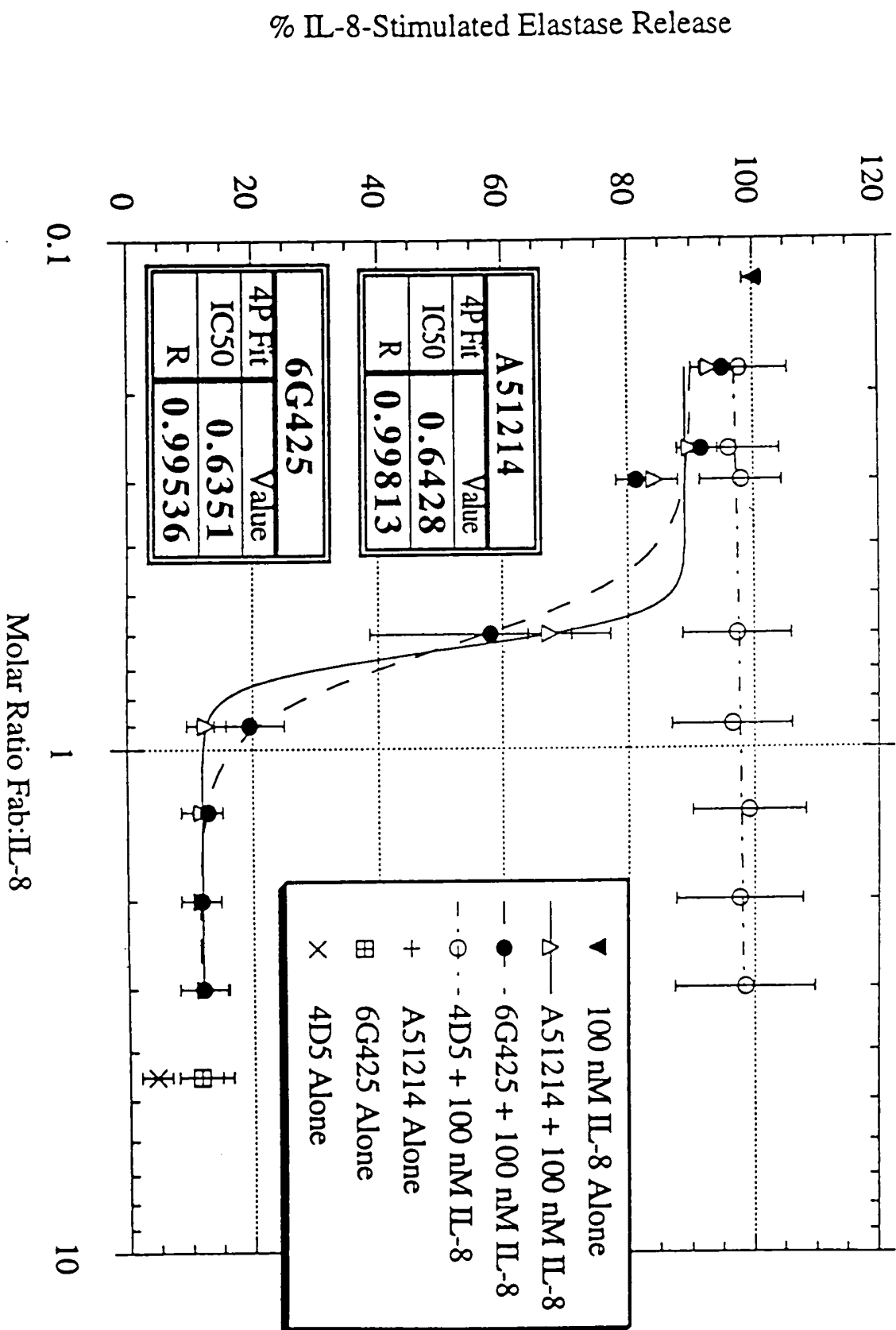
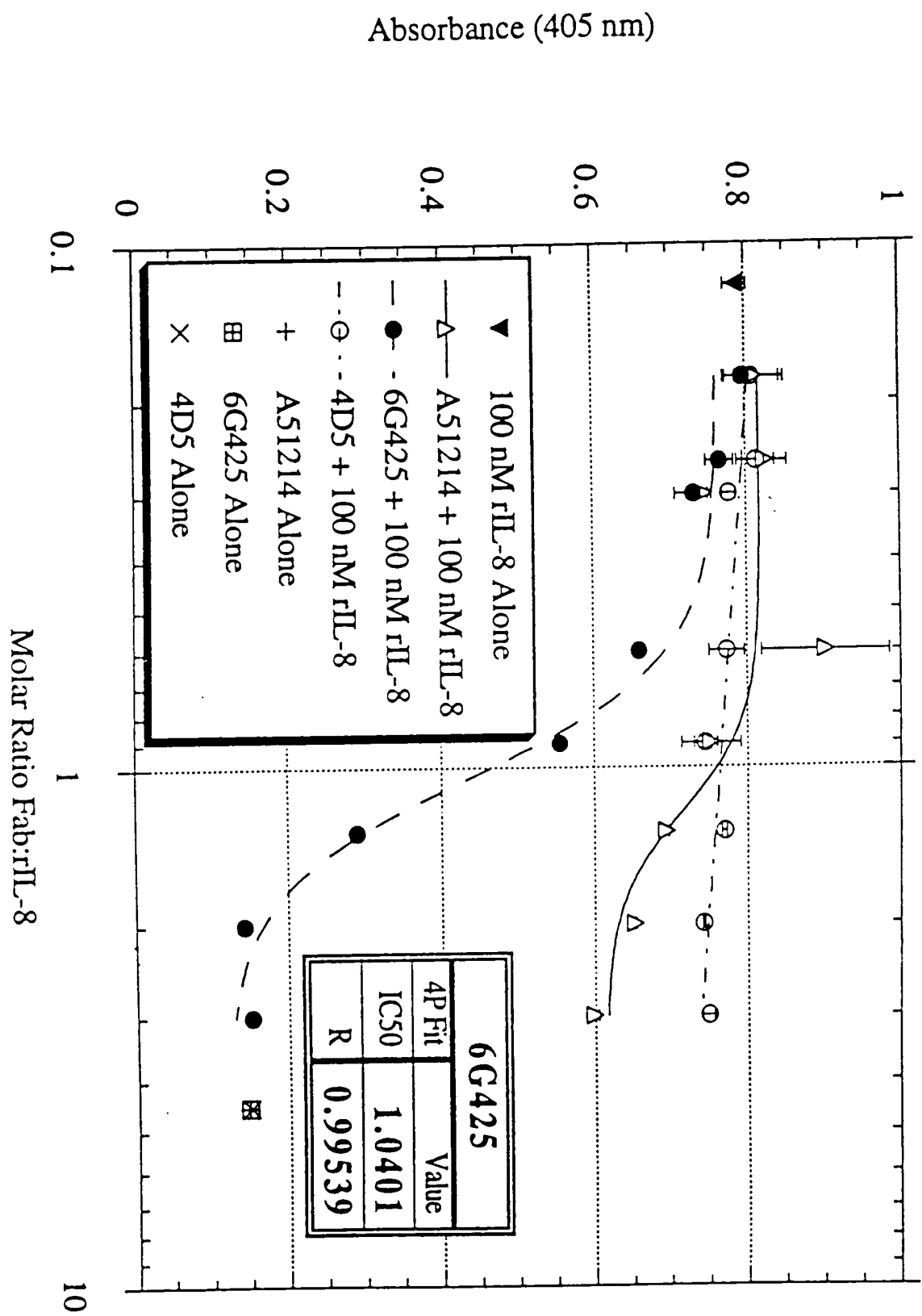


FIG. 10



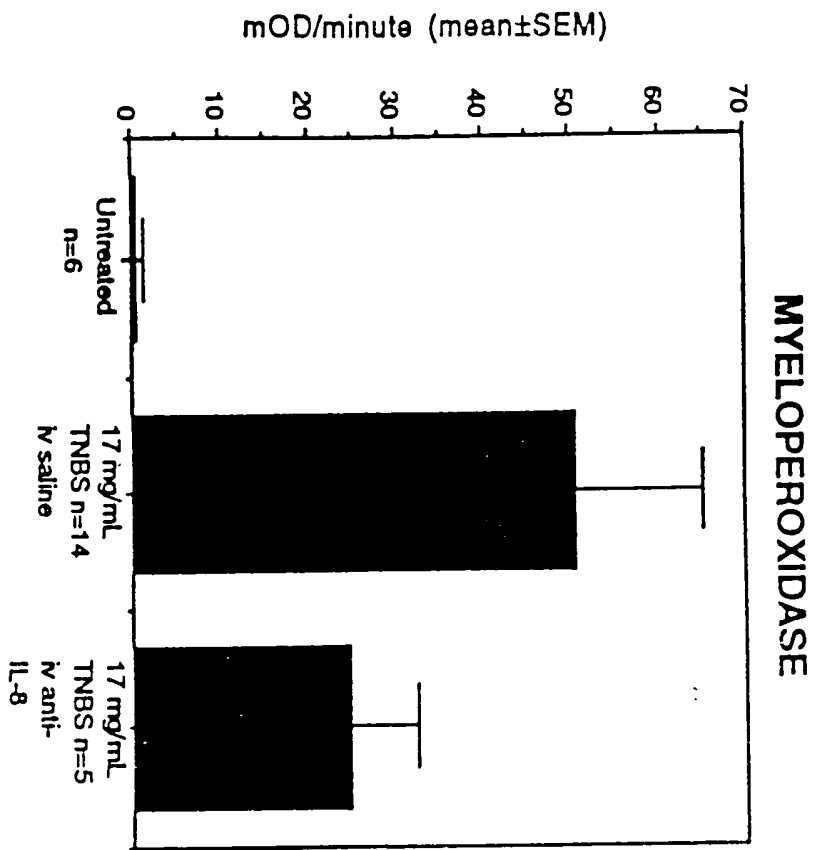


FIG. 11A

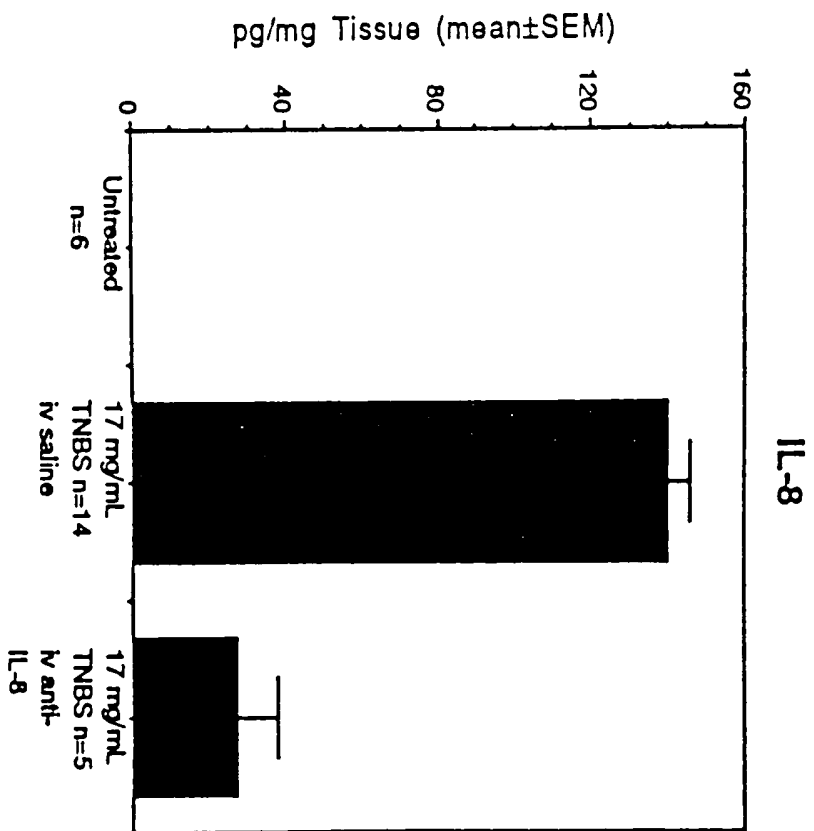


FIG. 11B

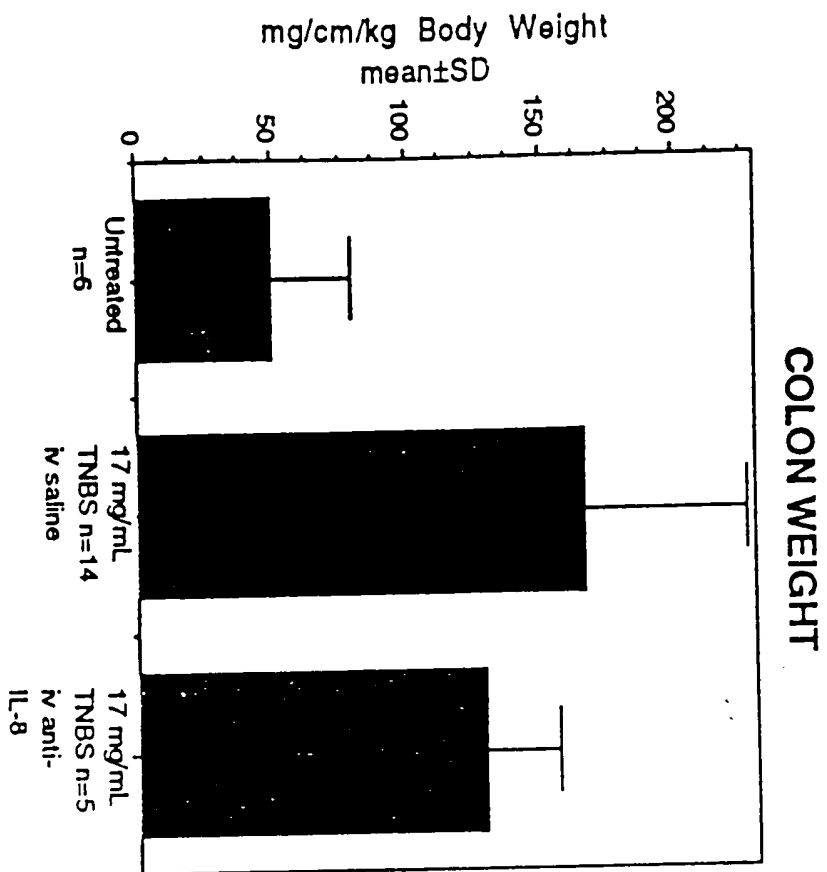


FIG. 11C

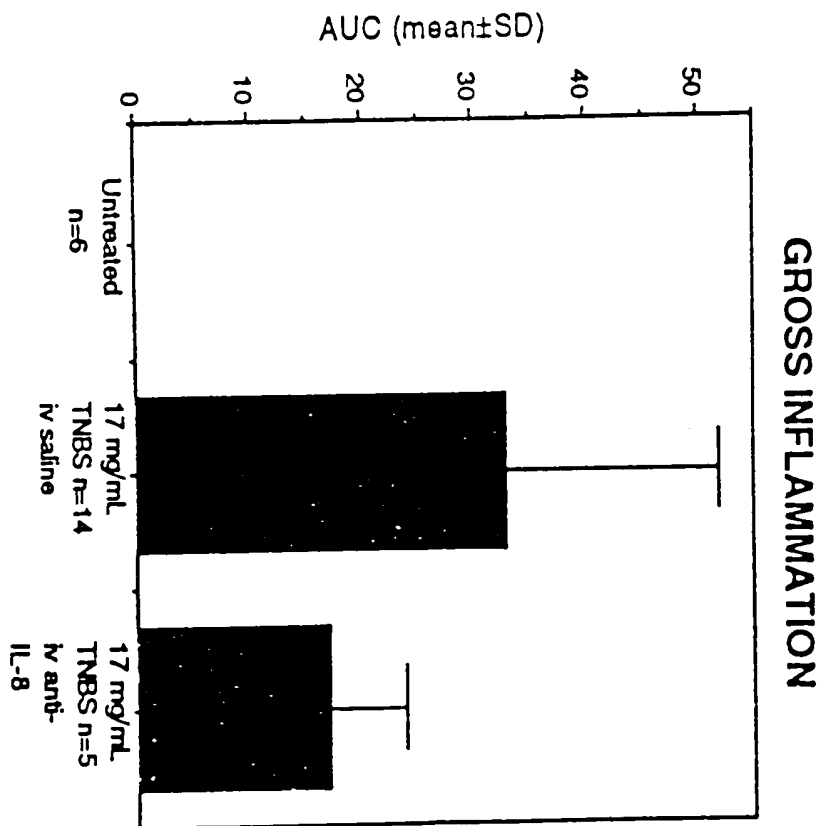


FIG. 11D

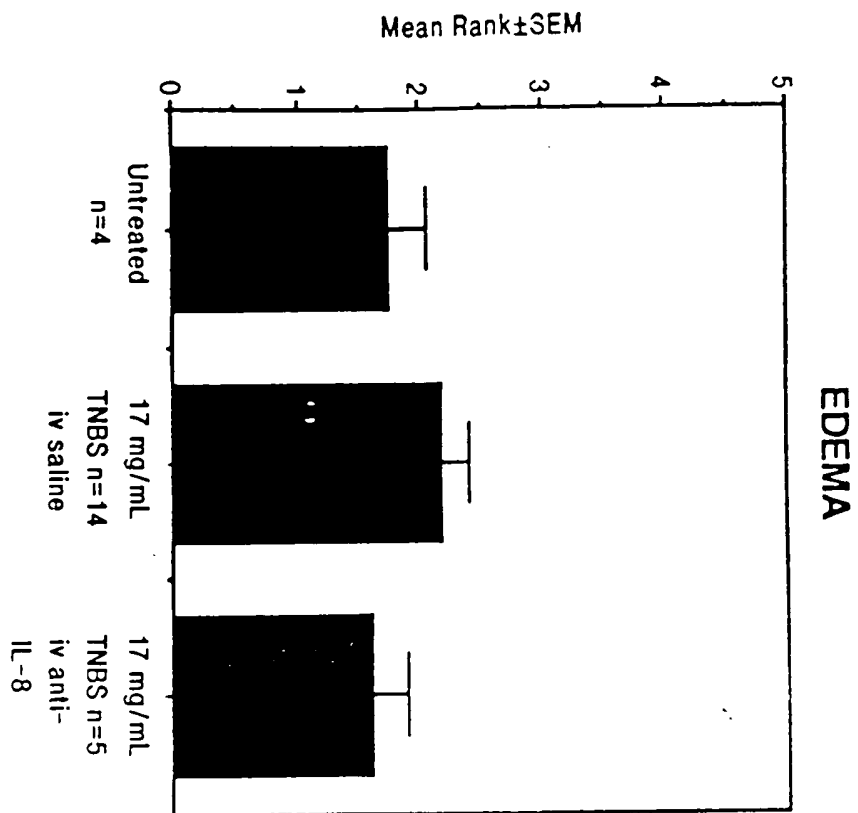


FIG. 11E

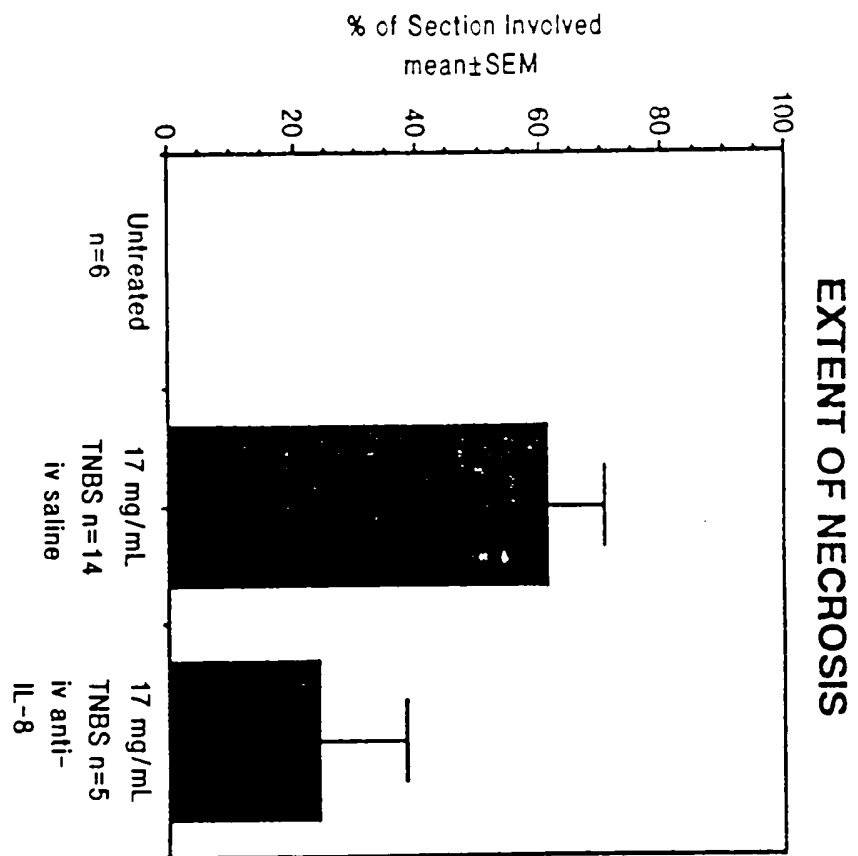


FIG. 11F

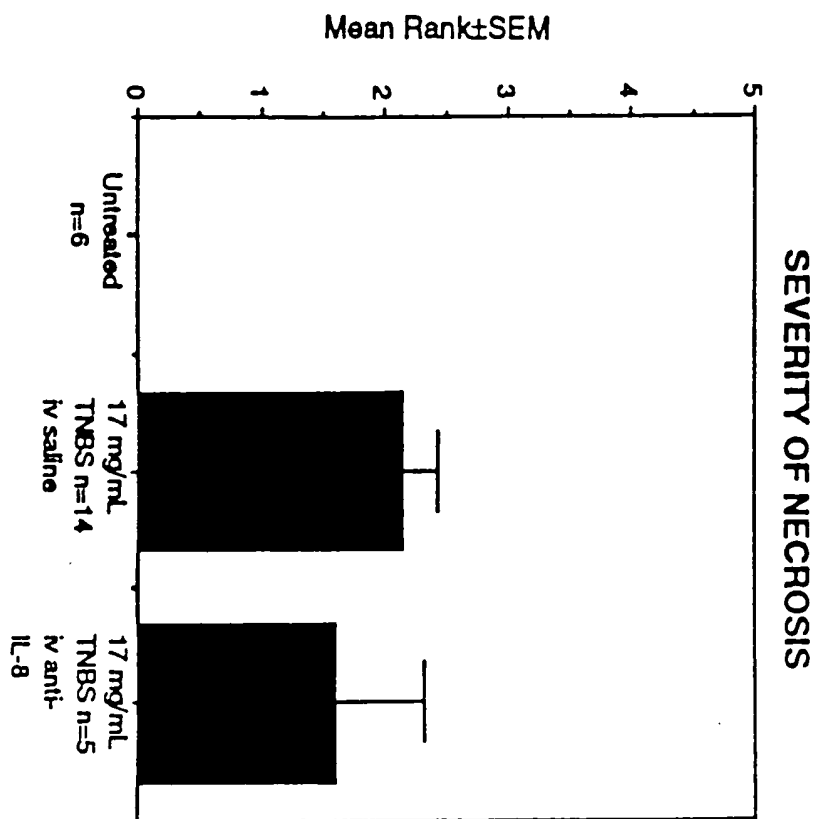


FIG. 11G

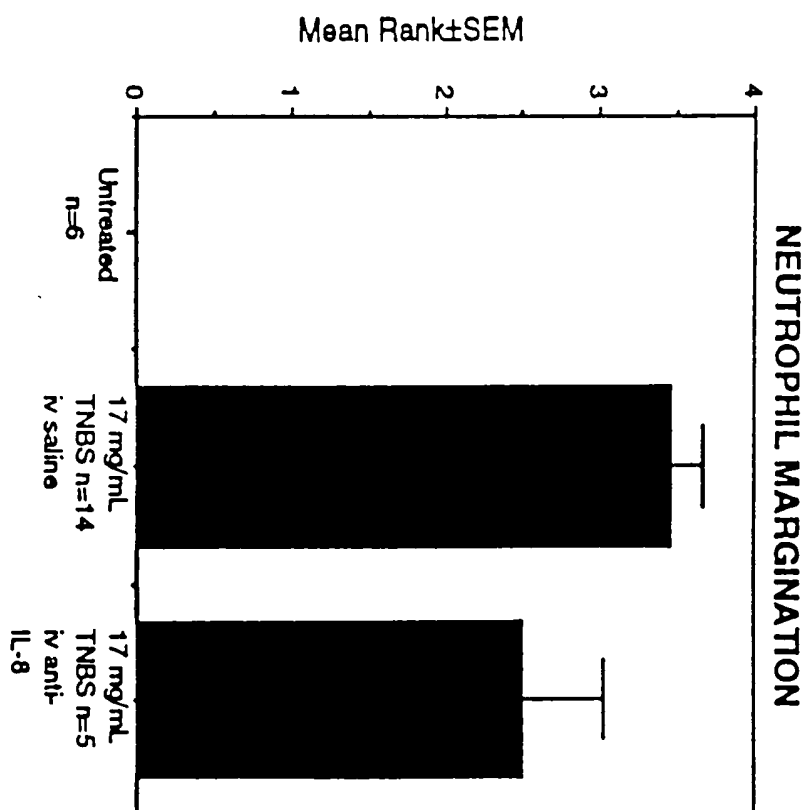


FIG. 11H

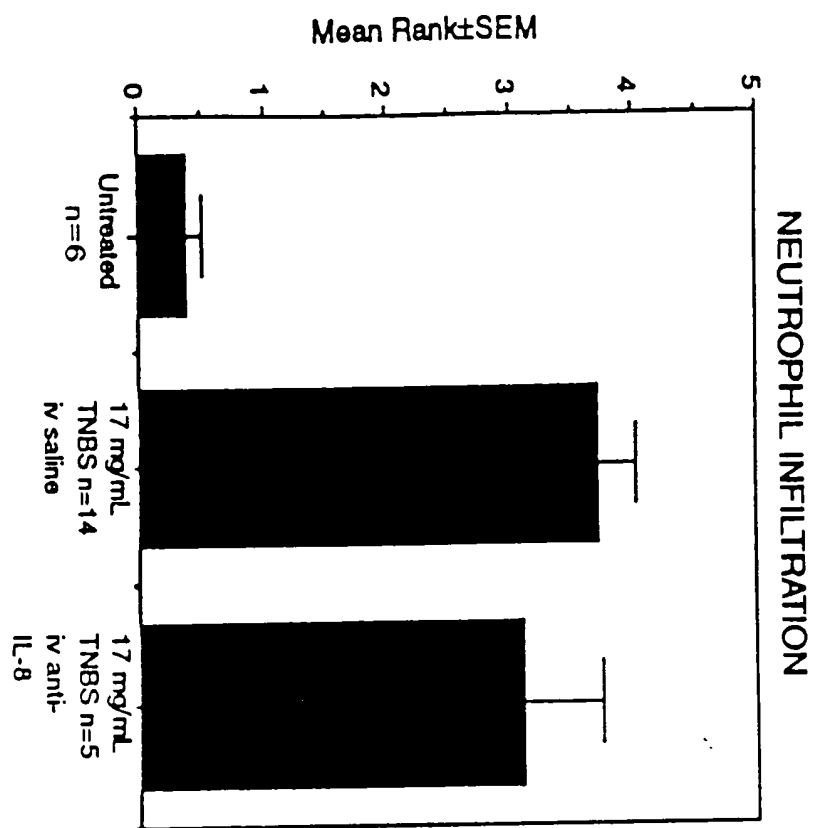


FIG. 11I

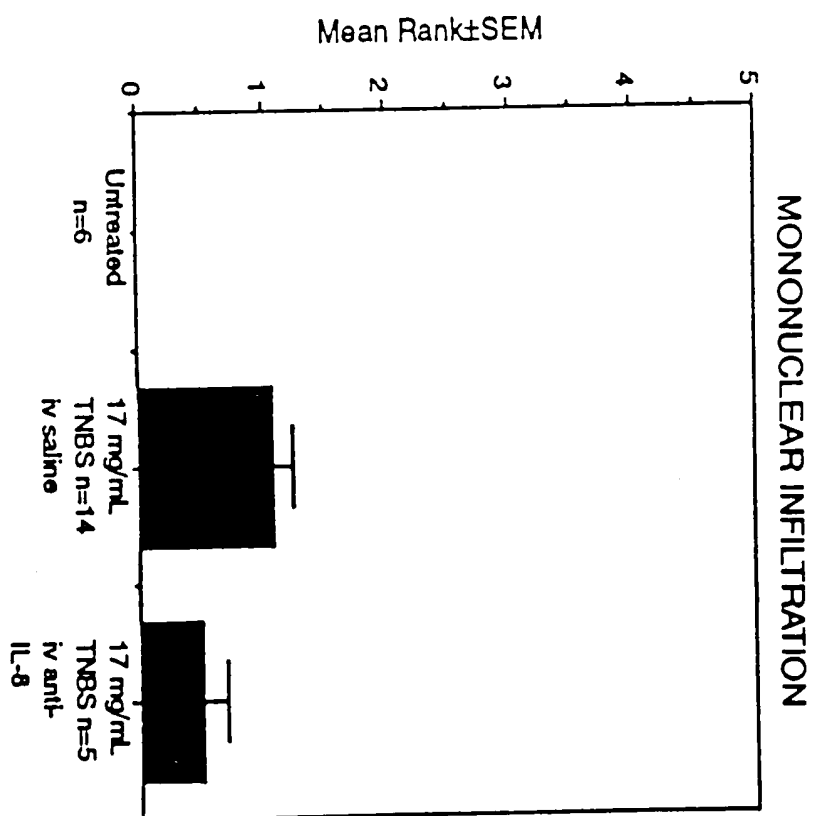
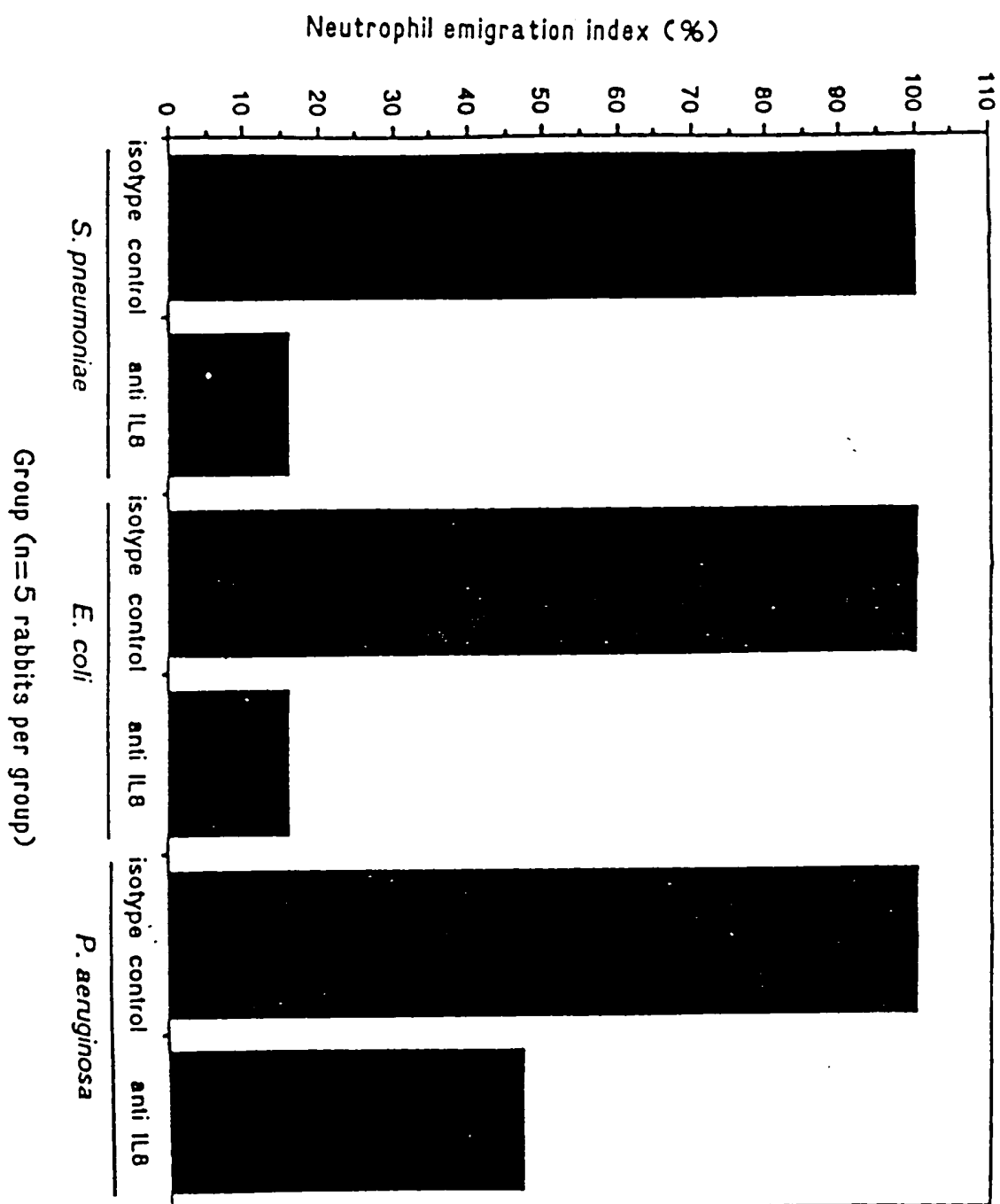


FIG. 11J

FIG. 12



Light chain Primers:

FIG. 13

MKLC-1, 22mer

5' CAGTCCAACTGTTCAAGGACGCC 3'

(SEQ ID NO: 1)

MKLC-2, 22mer

5' GTGCTGCTCATGCTGTAGGTGC 3'

(SEQ ID NO: 2)

MKLC-3, 23mer

5' GAAGTTGATGTTCTTGAGTGGC 3'

(SEQ ID NO: 3)

Heavy chain Primers:

IGG2A-1, 24mer

5' GCATCCTAGAGTCACCGAGAGCC 3'

(SEQ ID NO: 4)

IGG2A-2, 22mer

5' CACTGGCTCAGGGAATAACCC 3'

(SEQ ID NO: 5)

IGG2A-3, 22mer

5' GGAGAGCTGGGAGGTTGTCAC 3'

(SEQ ID NO: 6)

5' GCTCTTCGAATG GTGGGAAGATGATACAGTTGGTGC 3' (SEQ ID NO:10)

SL001B 37 mer

Light chain reverse primer

(SEQ ID NO:7)
(SEQ ID NO:8)
(SEQ ID NO:9)

5' ACAACGCGTACGCT GACATCGTCATGACCCAGTC 3'
T T
T
A

SL001A-2 35 mer

Light chain forward primer

FIG. 14

Heavy chain forward primer

FIG. 15

SL002B 39 mer

5' CGATGGCCCCG ATAGACCGATGGGCTGTTGTTGGC 3' (SEQ ID NO:11)

(SEQ ID NO:12)
(SEQ ID NO:13)
(SEQ ID NO:14)

T
G
A

Heavy chain reverse primer

SL002B 39-MER

5' CGATGGCCCCG ATAGACCGATGGGCTGTTGTTGGC 3' (SEQ ID NO:11)

(SEQ ID NO:15)
(SEQ ID NO:14)
(SEQ ID NO:13)

T
A
G

1 GACATTGTCA TGACACAGTC TCAAAATTC ATGTCACAT CAGTAGGAGA CAGGTCAGC
CTGTAACAGT ACTGTGTCAG AGTTTTTAAG TACAGGTGTA GTCATCCTCT GTCCAGTCG
1 D I V M T Q S Q K F M S T S V G D R V S

61 GTCACCTGCA AGGCCAGTCA GAATGTGGT ACTAATGTAG CCTGTATCA ACAGAAACCA
CAGTGACGT TCCGGTCAGT CTACACCCA TGATTACATC GGACCATAGT TGTCTTGGT
21 V T C K A S O N V G T N V A W Y Q Q K P
* * * * *

CDR #1

121 GGGCAATCTC CTAAGCACT GATTTACTCG TCATCCTACC GGTACAGTGG AGTCCCTGAT
CCCGTAGAG GATTTCTGA CTAATGAGC AGTAGGATGG CCATGTCACC TCAGGACTA
41 G Q S P K A L I Y S S S Y R Y S G V P D
* * * * *

CDR #2

181 CGCTTCACAG GCAGTGATC TGGACAGAT TTCACTCTCA CCATCAGCCA TGTGCAGTCT
GGAGAGTGC CGTCACCTAG ACCCTGTCTA AAGTGAGAGT GGTAGTCGT ACACGTCAGA
61 R F T G S G S G T D F T L T I S H V Q S

241 GAAGACTTGG CAGACTATT CTGTCAGCAA TATAACATCT ATCCTCTCAC GTTCGGTCCCT
CTTCTGAACC GTCTGATAA GACAGTCGTT ATATTGTAGA TAGGAGAGTG CAAGCCAGGA
81 E D L A D Y F C Q Q Y N I Y P L T F G P
* * * * *

CDR #3

301 GGGACCAAGC TGGAGTTGAA ACGGGCTGAT GCTGCACCAC CAACTGTATC CATCTTCCCA
CCCTGGTTCG ACCTCAACTT TGCCCGACTA CGACGTGGTG GTGACATAG GTAGAAGGT
101 G T K L E L K R A D A A P P T V S I F P

BstBI

361 CCAATTCGAA (see MD No: 16)
GGTAAGCTT

121 P F E (see MD No: 17)

FIG. 16

1 TTCTATTGCT ACAACGCGT ACCGTGAGT GCAGCTGGTG GAGTCTGGG GAGGCTTAGT
AAGATAACGA TGTTGCGCA TCGCACTCCA CGTCGACCA CTAAGACCCC CTCGGAATCA
E V Q L V E S G G G L V

61 GCGGCGCTGA GGTCCCTGA AACTCTCTG TGCAGCCTCT GATTTCATAT TCAGTAGTTA
CGGCGGACCT CCCAGGACT TTGAGAGGAC ACGTCGAGA CCTAAGTATA AGTCATCAAT
G S L K L S C A A S G F I F S S X

CDR #1

121 TGGCATGCT TGGTTGCGC AGACTCCAGG CAAGAGCCTG GAGTTGGTCG CAACCATTA
ACCGTACAGA ACCAAGCGG TCTGAGGTCC GTCTCGGAC CTCAACCAAGC GTTGGTAATT
G M S W V R Q T P G K S L E L V A T I N

181 TAATAATGGT GATAGCACT ATTATCCAGA CAGTGTGAAG GCGCGATTCA CCATCTCCCG
ATTATTACCA CTATCGTGA TAATAAGTCT GTCACTCTC CCGGCTAAGT GGTAGAGGCG
N N G D S T Y Y P D S V K G R F T I S R

CDR #2

241 AGACAATGCC AAGAACCCT TGTACCTGCA AATGAGCAGT CTGAAGTCTG AGGACACAGC
TCTGTACCG TTCTTGTGCG ACATGGAGCT TTACTCGTCA GACTTCAGAC TCCTGTGTCG
D N A K N T L Y L Q M S S L K S E D T A

301 CATGTTTAC TGTGCAAGAG CCTCATTAAG TTCGGCTACT TGGTTGGTT ACTGGGCGCA
GTACAAATG ACACGTTCTC GAGAGTAATC AAGCCGATGA ACCAACCA TGAACCCCGT
M F Y C A R A L I S S A T W F G Y W G Q

CDR #3

361 AGGACTCTG GTCACTGCT CTGCAGCCAA AACAAACGCC CCATCTGCT
TCCCTGAGAC CAGTGACAGA GACGTCGGTT TTGTTGTCGG GGTAGACAGA
G T L V T V S A A K T T A P S V Y

ApaI

411 ATCCGGG (Seq ID No: 18)

TAGGCC

130 P (Seq ID No: 19)

FIG. 17

FIG. 18

VL.front 31-MER
5' ACAAAGCGTACCGCTGATATCGTCATGACAG 3' (SEQ ID NO: 26)
VL.rear 31-MER
5' GCAGCATCAGCTCTTCGAAGCTCCAGCTTGG 3' (SEQ ID NO: 21)
VH.front.SPE 21-MER
5' CCACTAGTACGCAAGTTACG 3' (SEQ ID NO: 22)
VH.rear 33-MER
5' GATGGGCCCTTGCTGGAGGCTGCAGAGACAGTG 3' (SEQ ID NO: 23)

216

O
TAA
TATT

(seq ID 10:24)

FIG. 19

1 ATGAAGAAGA ATATCGCATT TCTCTTGA TCTATGTTG TTTTCTAT TCCTACAAAC
-23 M K K N I A F L L A S M F V F S I A T N
61 GCGTAGCGTG ATATCGTCAT GACACAGTCT CAATAATTCA TGTCCACATC AGTAGGAGAC
-3 A Y A D I V M T Q S Q K F M S T S V G D
121 AGGGTCAGCG TCACCTGCAA GGCCAGTCAG AATGTGGTA CTAATGTAGC CTGGTATCAA
TCCAGTCGC AGTGCAGCTT CCGGTCACTC TTACACCAT GATTACATCG GACCATAGTT
18 R V S V T C K A S O N V G T N V A W Y Q

CDR #1

181 CAGAAACCAG GCGAATCTCC TAAAGCACTG ATTACTCGT CATCCTACCG GTACAGTGA
38 Q K P G Q S P K A L I Y S S Y R Y S G
GTCTTTGTC CCGTTAGAGG ATTTGCTGAC TAAATGAGCA GTAGATGGC CATGTCACCT

CDR #2

241 GTCCTGATC GCTTCACAGG CAGTGGATCT GGACAGATT TCACCTCAC CATCAGCCAT
CAGGAGCTAG CGAAGTGTCC GTACCTAGA CCTGTCTAA AGTAGAGTG GTAGTCGGTA
58 V P D R F T G S G S G T D F T L T I S H
301 GTGAGTCTG AAGACTTGGC AGACTATTTC TGTACGCAAT ATAACATCTA TCCTCTCAG
CAGCTCAGAC TTCTGAACCG TCTGATAAAG ACAGTCGTTA TATTGTAGAT AGGAGAGTGC
78 V Q S E D L A D Y F C Q Q X N I Y P L T

CDR #3

361 TTCGGTCTG GGAACCAAGT GGAGCTTCGA AGAGCTGTGG CTGACCATC TGTCTTCATC
AAGCCAGGAC CCTGGTTGCA CCTCGAAGCT TCTCGACACC GACGTGGTAG ACAGAAGTAG
98 F G P G T K L E L R R A V A A P S V F I
421 TTCGGCCAT CTGATGAGCA GTTGAATCT GGAATGCTT CTGTTGTGTC CTGCTGAAT
AAGGGCCGTA GACTACTCGT CAACCTTAGA CCTTGACGAA GACAACACAC GAGCGACTTA
118 F P P S D E Q L K S G T A S V V C L T N
481 AACTTCTATC CCAGAGAGCG CAAGTACAG TGAAGGTGG ATAAAGCCCT CCAATCGGT
TTGAAGATAG GGTCTCTCCG GTTTCATGTC ACCTTCACC TATTGGCGGA GGTAGGCCA
138 N F Y P R E A K V Q M K V D N A L Q S G
541 AACTCCAGG AGAGTGTAC AGAGCAGGAC AGCAAGACA GCACCTACAG CCTCAGCAGC
TTGAGGGTCC TCTCAGAGTG TCTGCTCTG TCGTTCCTGT CGTGAGTGTG GAGTCCGTG
158 N S Q E S V T E Q D S K D S T Y S L S S
601 ACCCTGACCG TGAGCAAGC AGACTACGAG AAACACAAAG TCTACGCCCTG CGAAGTACAC
TGGAAGTGG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGCCGAC GCTTCAGTGG
178 T L T L S K A D Y E K H K V Y A C E V J
661 CATCAGGGCC TGAGCTCGCC CGTCAAAAG AGCTTCAACA GGGAGAGTG
GTAGTCCCGG ACTCGAGCGG GCAGTGTTC TCGAAGTTGT CCCCTCTCAC

198 H Q G L S S P V T K S F N R G E C (seq ID 10:25)

FIG. 20A

1 ATGAAAAGA ATATCGATT TCTTCTTGA TCTATGTTCC TTTTTCAT TCCTACAAAC
 -23 M K K N I A F L L A S M F V F S I A T N
 61 CGGTACGCTG AGTGCAGCT GGTGAGTCT GGGGAGGCT TAGTCCGCTC TGAGGGTCC
 -3 A Y A E V Q L V E S G G G L V P P G G S
 121 CTGAACCTCT CCTGTGCAGC CTCTGATTG ATATTGAGTA GTTATGGCAT GTCTTGGGTT
 18 L K L S C A A S G F I F S S X G M S W V
 CDR #1
 181 CGCCAGACTC CAGGCAAGAG CCTGAGATTG GTCCGAACA TTAATAATAA TGGTGATAGC
 38 R Q T P G K S L E L V A T I N N N G D S
 241 ACCTATTATC CAGACAGTGT GAAAGGCCGA TTCACCATCT CCCGAGACAA TGCCAGAAC
 58 T Y Y P D S V K G R F T I S R D N A K N
 CDR #2
 301 ACCCTGTACC TGCATAAGAG CAGTCTGAAG TCTGAAGACA CAGCCATGTT TTACTGTGCA
 78 T L Y L Q M S S L K S E D T A M F Y C A
 361 AGAGCCCTCA TTAGTTCGGC TACTTGTTT GGTACTGGG GCCAAGGAG TCTGCTCACT
 98 R A L I S S A T W F G Y W G Q G T L V T
 CDR #3
 421 GTCTCTGAG CCTCCACCA GGGCCCATCG GTCTTCCCC TGCCACCCTC CTCGAAGAG
 118 V S A A S T K G P S V F P L A P S S K S
 481 ACCTCTGGG GCACAGCGGC CCTGGGCTG CTGGTCAAG ACTACTTCCC CGAACCGGTG
 138 T S G G T A A L G C L V K D Y F P E P V
 541 ACGGTGTCCT GGAACCTCAGG CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCTTA
 158 T V S W N S G A T T GGGGACTGG TCGCCGACG TGTGGAAGG CCGACAGAT
 601 CAGTCCCTCAG GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG CAGCTTGGG
 178 Q S S G T Y S L S S V V T V P S S L G
 GTCAGGAGTC CTGAGATGAG GGAGTGGTCC CACCACTGGC ACGGAGGTC GTGGAACCCG

FIG. 20B

661 ACCGACCT ACATCTGCAA CGTGAATCAC AAGCCCAAGCA ACACCAAGGT GGACAAGAAA
TGGTCTGGA TGTAAGCGTT GCACTTAGTG TTCCGGTCCG TGTTGGTTCCA CCTGTTCTTT
198 T Q T Y I C N V N H K P S N T K V D K K
721 GTTGAGCCCA AATCTTGTGA CAAACTCAC ACATGA (SEQ ID NO: 26)
CAACTCGGGT TTAGAACACT GTTTGAGTG TGTAAT (SEQ ID NO: 27)
218 V E P K S C D K T H T O

FIG. 21

Light chain Primers:

MKLC-1, 22mer

5' CAGTCCAACTGTTGAGGAGCC 3'

(SEQ ID NO: 1)

MKLC-2, 22mer

5' GTGCTGCTCATGCTGTAGGTGC 3'

(SEQ ID NO: 2)

MKLC-3, 23mer

5' GAAGTTGATGTTCTGTGAGTGGC 3'

(SEQ ID NO: 3)

Heavy chain Primers:

IGG2AC-1, 24mer

5' GCATCCCTAGAGTCACCGAGGAGCC 3'

(SEQ ID NO: 4)

IGG2AC-2, 22mer

5' CACTGGCTCAGGGAATAACCC 3'

(SEQ ID NO: 5)

IGG2AC-3, 22mer

5' GGAGAGCTGGGAAGTGTGCAC 3'

(SEQ ID NO: 6)

FIG. 22

5' AGA TGT CAA TTG CTC ACT GGA TGG TGG GAA GAT GG 3' (SEQ ID NO: 31)

6G4.lght.Mun 35-MER

Light chain reverse primer

(SEQ ID NO: 28)
(SEQ ID NO: 29)
(SEQ ID NO: 30)

A T A
T T A

T T

5' CCAATGCATACGCT GAC ATC GTG ATG ACC CAG ACC CC 3' (SEQ ID NO: 28)

6G4.lght.Nsi 36-MER

Light chain forward primer

FIG. 23

Heavy chain forward primer
 6G4.heavy.Mlu 32-MER
 5' CAAACCGGTACGCT GAG ATC CAG CTG CAG CAG 3' (SEQ ID NO: 32)
 C T

Heavy chain reverse primer
 SL002B 39-MER
 5' CGATGGGCCCCG ATAGACCGATGGGCTGTTGTTGGC 3' (SEQ ID NO: 11)
 T A G
 (SEQ ID NO: 15)
 (SEQ ID NO: 14)
 (SEQ ID NO: 13)

FIG. 24

70 G ATATCGTGAT GACACAGACA CCATCTCCG TGCCGTGACG TCTTGAGAT
C TATAGCACTA CTGTGCTGT GGTGAGAGG ACGGACAGTC AGAACCTCTA
I D I V M T Q T P L S L P V S L G D

121 CAGGCCTCCA TCTCTTGACG ATCTAGTCAG AGCCTTGAC AGGTATGCG AAACACCTAT
GTCCGGAGGT AGAGAACGTC TAGATCAGTC TCGGAACATG TGCCATAACC TTTGTGATA
18 Q A S I S C R S S O S L V H G I G N T Y

CDR #1

181 TTACATTGGT ACCTGCAGAA GCCAGGCCAG TCTCCAAAGC TCCTGATCTA CAAAGTTCC
AATGTAACCA TGGACGTCCT CGGTCCGGTC AGAGGTTTCG AGGACTAGAT GTTCAAGG
38 L H W Y L Q K P G Q S P K L L I Y K V S

CDR #2

241 AACCGATTT CTGGGCTCC AGACAAGTTC AGTGCAGTC GATCAGGAC AGATTTACGA
TTGGCTAAAG GACCCAGGG TCTGTCCAG TCACCGTCAC CTAGTCCCTG TCTAAAGTGT
58 N R F S G V P D R F S G S G S G T D F T

301 CTAGGATCA GCAGAGTGA GGCTGAGGAT CTGGGACTTT ATTTCTGCTC TCAAGTACA
GAGTCCCTAGT CGTCTCACT CGGACTCCTA GACCCCTGAA TAAAGACGAG AGTTTCATGT
78 L R I S R V E A E D L G L Y F C S Q S L

CDR #3

361 CATGTTCCCG TCACGTTCCG TGCTGGGACC AAGCTGGAGC TGAAGAAGGGC TGAATGCTGA
GTACAAAGCG AGTGCAGGCC ACGACCCCTGG TTCGACCTCG ACTTTGCCCG ACTACGACGT
98 H V P L T F G A G T K L E L K R A D A A

MunI

421 CCAACTGTAT CCATCTTCCC ACCATCCAGT GAGCAATTGA
(SEQ ID NO: 34)
GGTTGACATA GGTGAGAGG TGGTAGGTC CTCGTTAACT
118 P T V S I F P P S S E Q L K
(SEQ ID NO: 35)

FIG. 25

70 G AGATTGAGCT GCAGCAGTCT GGACCTGAGC TGATGAAGCC TGGGGCTTCA
 C TCTAAGTCGA CGTCGTCAGA CCTGAGCTCG ACTACTTCGG ACCCGAAGT
 1 E I Q L Q S G P E L M K P G A S

121 GTGAAGATAT CCTGCAAGCC TTCTGGTTAT TCATTCAAGTA GCCACTAAT GCACCTGGGTG
 CACTTCTATA GGACGTTCCG AAGACCAATA AGTAAGTCAT CGGTGATGTA CGTGACCCAC
 18 V K I S C K A S G Y S F S H Y M H W V

CDR #1

181 AAGCAGAGCC ATGGAAGAAG CCTTGAGTGG ATTGGCTACA TTGATCCCTC CAATGGTGAA
 TTCGTCTCGG TACCTTTCTC GGAACCTCAC TAACCGATGT AACTAGGAAG GTTACCACTT
 38 K Q S H G K S L E W I G Y I D P S N G E

CDR #2

241 ACTACTTACA ACCAGAAATT CAAGGGCAAG GCCACATTGA CTGTAGAACA ATCTTCAGC
 TGATGAATGT TGGTCTTTAA GTTCCCGTTC CGGTGTAAT GACATCTGTG TAGAAGGTG
 58 T T Y N Q K F K G K A T L T V D T S S S

301 ACAGCCAAAG TGCATCTCAG CAGCCTGACA TCTGATGACT CTGCACTCTA TTTCTGTGA
 TGTCCGTTGC ACGTAGAGTC GTCCGACTGT AGACTACTGA GACGTCAGAT AAAGACACGT
 78 T A N V H L S S L T S D D S A V Y F C A

361 AGAGGGGACT ATAGATACAA CGGCGACTGG TTTTTCGATG TCTGGGGCCG AAGGACCAAG
 TCTCCCTGA TATCTATGTT GCCGCTGACC AAAAAGCTAC AGACCCCGCG TCCCTGGTGC
 98 R G D Y R Y N G D W F F D V W G A G T T

CDR #3

421 GTACCCGCTCT CCTCCGCCAA AACCGACAGC CCCATCGGTC TATCCGGGCC
 CAGTGCACGA GGAGCGCGAT TTGGCTGTCG GGTAGCCAG ATAGCCCGCG
 118 V T V S S A K T D S P I G L S G P

471 CATC (Seq ID No: 36)
 GTAG
 135 I (Seq ID No: 37)

FIG. 26

5' CTTGGTGAGCGCGGAGAGACG 3' (see ID No: 38)

SYN.Apa 22 MER

5' GTACCCGCT CCTCCGCTC CACCAAGGC C 3' (see ID No: 40)

SYN.BstEII 31 MER

5' GAAACGGGCTGTTGCTGCACCAACTGTATTCATCTCC 3' (see ID No: 39)

DS/VF 38MER

Mutagenesis Primer for 6G425VL

5' CTTGGTGAGCGCGGAGAGACG 3' (see ID No: 38)

FIG. 27A

1 ATGAAGAATA ATATCCGATT TCTTCTTCA TCTATGTTCC TTTTCTTAT TGCTACAAT
TACTTCTTCT TATAGCGTAA AGAAGAAGCT AGATACAAGC AAAAAGATA AGCATGTTTA
-23 M K K N I A F L L A S M F V F S I A T N
61 GCATACGCTG ATATCGTGAT GACACAGACA CCACTCTCC TGCTGTCA TCTTGAGAT
CGTATCGGAC TATAGCACTA CTGTGTCTGT GGTGAGAGG AGGACAGTC AGAACCTTA
-3 A Y A D I V M T Q T P L S L P V S L G D
121 CAGGCTCCA TCTCTTGCAG ATCTAGTCAAG AGCTTGTAC AGGTATTGG AAACACCTAT
GTCCGAGGT AGAGAAGTC TAGATCACTC TCAGAACATG TGCCATAAC TTTGTGATA
18 Q A S I S C R S S O S L V H G I G N T X
CDR #1
181 TTACATTGGT ACCTGCAGAA GCCAGGCCAG TCTCCAAGC TCCGTATCTA CAAAGTTCC
AATGTAAACA TGACGTTCTT CGGTCCGCTC AGAGGTTCC AGGACTAGAT GTTCAAGG
38 L H W Y L Q K P G Q S P K L L I Y K V S
CDR #2
241 AACGATTTT CTGGGTTCC AGACAGGTTC AGTGGCAGTG GATCAGGGAC AGATTTCACA
TTGGTTAAAG AACCCAGGG TCTGTCCAAG TCACCGGTAC CTAGTCCCTG TCTAAAGTGT
58 N R F S G V P D R F S G S G S G T D F T
301 CTCAGATCA GCAGAGTGA GGTGAGAT CTGGGACTTT ATTTCTGCTC TCAAGTACA
GAGTCCCTAGT CGTCTCACT CGGACTCTA GACCTGAAA TAAAGAGAG AGTTTCATGT
78 L R I S R V E A E D L G L Y F C S Q S L
CDR #3
361 CATGTTCCG TCACGTTCC TGCTGGACC AAGCTGGAGC TGAACGGGC TGTTGCTGA
GTACAAGGC AGTCCAAGC AGAACCTTG TTGCACTCG ACTTGCCCG ACAACGAGCT
98 H V P L T F G A G T K L E L K R A V A A
421 CCACTGTAT TCATCTTCC ACCATCCAGT GAGCAATTGA AATCTGGAAC TGCTCTGTT
GGTGACATA AGTGAAGG TGTTAGTCA CTGTTAAT TTAGACCTG ACGGAGACAA
118 P T V F I F P P S S E Q L K S G T A S V
481 GTGCTCTG TGAATACTT CTATCCAGA GAGGCCAAG TACAAGTGA GGTGATTAAC
CACACGGAG ACTTATTGA GATAGGTTCT CTCGGTTCT ATGTACCTT CCACTTATG
138 V C L T N N F Y P R E A K V Q W K V D N
541 GCGTCAAT CCGTAACTC CCAAGAGAGT GTCACAGAGC AGGACAGCA GACAGCACC
CGGAGGTTA GCCCATTTAG GGTCTCTCA CAGTGTCTCG TCTGTCTGTT CCTGTCTG
158 A L Q S G N S Q E S V T E Q D S K D S T
601 TACAGCTCA GACGACCTT GACGTGAGC AAAGCAGCT ACAGAAACA CAAAGTCTAC
ATGTCCGAGT CGTCCGAGC GTCCGCTGA TCTCTTGT GTTTCAGATG
178 Y S L S S T L T L S K A D Y E K H K V Y

661 GCCTGCCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
 CGGACGCTTC AGTGGGTAGT CCCGGACTCG AGCGGGCAGT GTTCTCGAA GTTGTCCTCCT
 198 A C E V T H Q G L S S P V T K S F N R G

721 GAGTGTTAA (SEQ ID NO: 41)
 CTCACAATT
 218 E C O (SEQ ID NO: 42)

FIG. 27B

FIG. 28A

1 ATGAAAAGA ATATCGCAT TCTTCTGCA TCTATGTTG TTTTCTAT TGCTACAAC
 -23 M K K N I A F L L A S M F V F S I A T N
 61 GCGTACGCTG AGATTCACT GCAGCAGTCT GCACCTGAGC TGATGAAGC TGCGGCTTCA
 -3 A Y A E I Q L Q Q S G P E L M K P G A S
 121 GTGAAGATAT CCTGCAAGC TTCTGGTAT TCATTCACTA GCACTAGCTG
 CACTTCTATA GCAGCTTCCG AAGACCAATA AGTAAGTAT CGGTAGTATA CGTGACCCAC
 18 V K I S C K A S G Y S F S S H Y M H W V
 CDR #1
 181 AAGCAGAGCC ATGAAAGAG CCTTGAGTGG ATTGGCTTCA TTGATCCTTC CAATGGTGA
 TTGCTCTCGG TACCTTTCTC GGAATCTACC TAACCGATGT AACTAGGAAG GTTACCACTT
 38 K Q S H G K S L E W I G Y I D P S N G E
 CDR #2
 241 ACTACTTACA ACCAGAATT CAAGGGCAAG GCCACATTGA CTGTAGACAC ATCTTCCAGC
 TGATGAATGT TGGTCTTTAA GTTCCCGTTC CGGTGTAAT GACATCTGTG TAGAAGGTG
 58 T T Y N Q K F K G K A T L T V D T S S S
 301 ACAGCCAACG TGATCTCAG CAGCCTGACA TCTGATGACT CTGCAGTCTA TTTCTGTGA
 TGTCGGTTGC ACGTAGATC GTCCGACTGT AGACTACTGA GACGTCAAGT AAAGACACGT
 78 T A N V H L S S L T S D D S A V Y F C A
 361 AGAGGGGACT ATGATACAA CGCGGACTGG TTTTTCGATG TCTGGGGCCG AGGACCCAGC
 TCTCCCTGA TATCTATGTT GCCGCTGACC AAAAAGCTAC AGACCCCGCG TCCCTGGTGC
 98 R G D Y R Y N G D W F F D V W G A G T T
 CDR #3
 421 GTACCGTCT CCTCCGCTC CACCAAGGC CCATCGGTCT TCCCGCTGCG ACCCTCTCC
 CAGTGGCAGA GGAGGGGAG GTGGTTCCCG GGTAGCCAGA AGGGGACCG TGGGAGGAGG
 118 V T V S S A S T K G P S V F P L A P S S
 481 AAGAGCACT CTGGGGCAC AGCGGCCCTG GGTGCTGCTG TCAAGGACTA CTTCGCCGA
 TTCTCGTGA GACCCCGCTG TCGCCGGGAC CCGACGAGC AGTTCTGTAT GAAGGGGCTT
 138 K S T S G G T A A L G C L V K D Y F P E
 541 CCGGTGACCG TGTGCTGAA CTCAGCGGCC CTGACCAAGC GCGTGCACAC CTTCGCCGCT
 GGCCACTGCC ACAGCACTT GAGTCCGCGG GACTGGTCCG CGACGCTGTG GAAGGGCCGA
 158 P V T V S W N S G A T T S G V H T F P A
 601 GTCTACAGT CCTCAGGACT CTACTCCCTC AGCAGCGTGG TGACCGTCCG CTCCAGCAGC
 CAGGATGTCG GAGTCCCTGA GATGAGGAG TCGTCCGACC ACTGCGCACCG GAGGTGCTCG
 178 V T Q S S G T X S L S S V V T V P S S S

661 TTGGGCACCC AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGAC
 AACCCTGGG TCTGATGTA GACGTGCAC TTAGTGTTCG GGTGTTGTG GTTCACCTG
 198 L G T Q T Y I C N V N H K P S N T K V D
 721 AAGAAGTTG AGCCCAATC TTGTGACAAA ACTCACACAT GA (SEQ ID NO: 43)
 TTCTTCAAC TCGGTTTAG AACACTGTTT TGAGTGTGA CT
 218 K K V E P K S C D K T H T O (SEQ ID NO: 44)

FIG. 28B

FIG. 29

Variable Light Chain Domain

6G425
F(ab)-1
humk1

DIQTPTPLSPVSLDQASISCRSSQSLVHIGICNTYLLHMYLQKPGQSPKLLIY
DIQTQSPSSLASVGDRTITICRSHGICNTYLLHMYLQKPGKAPKLLIY
DIQTQSPSSLASVGDRTITICFASRTI-----SKYLAWYQKPGKAPKLLIY

L1
++++++
=====

6G425
F(ab)-1
humk1

YKSNRPFSGVDFDRFSDSGSGTDFTLRIISRAVEADLGLVFCQSQSTHVPILTFCASTKLEKR
YKSNRPFSGVDFDRFSGSGSGTDFTLTSSLPEDFATYYCSQSSTHVPILTFGQGTKEIKR
YSGSTLESQVPSRFSRSGSGSGTDFTLTSSLPEDFATYYCQQHNEYPLTFGQGTKEIKR

L2
++++++
=====

L3
++++++
=====

(SEQ ID NO: 45)
(SEQ ID NO: 46)
(SEQ ID NO: 47)

Variable Heavy Chain Domain

6G425
F(ab)-1
humk1

EIQDQSGPELTKPGASVKISCKASGYSPFSSHYMHVAKQSHGKSLMI
EVQLVESGGGLVQPGGSLRLSCAASGYSFSSHYMHVWRQAPKGKLEW
EVQLVESGGGLVQPGGSLRLSCAASGYSFSGTGMWMWRQAPKGKLEW

H1
++++
=====

6G425
F(ab)-1
humk1

GYIDPSNGETTYNQKFKGKATLLTVDTSSSTAVHLSLTSDDSAVYFCAAARGDYRYNGDWFFDVWGAGT
GYIDPSNGETTYNQKFKGKRTTISRDNKNTLYLQHMNSLRAEDTAVYYCAARGIYFY-GTTFDYWGQGT
GMHPDSSETRYADSVKGRFTISRDNKNTLYLQHMNSLRAEDTAVYYCAARGIYFY-GTTFDYWGQGT

H2
++++++
=====

H3
++++++
=====

(SEQ ID NO: 48)
(SEQ ID NO: 49)
(SEQ ID NO: 50)

FIG. 30A

IC50~12nM

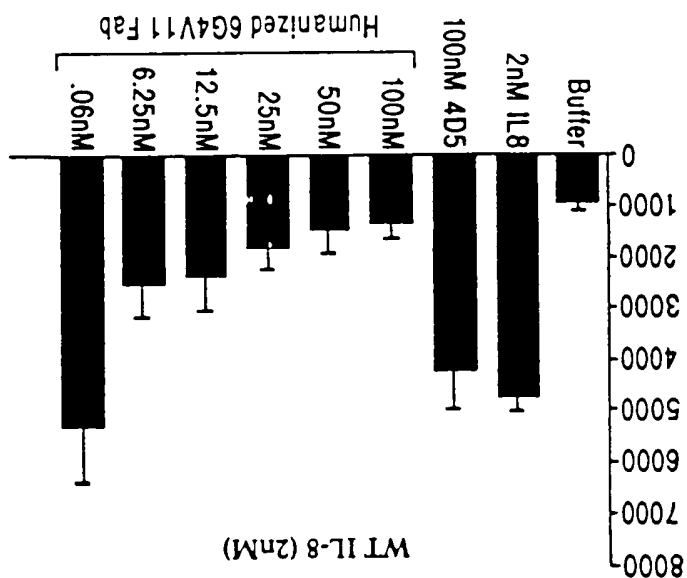


FIG. 30B

IC50~15nM

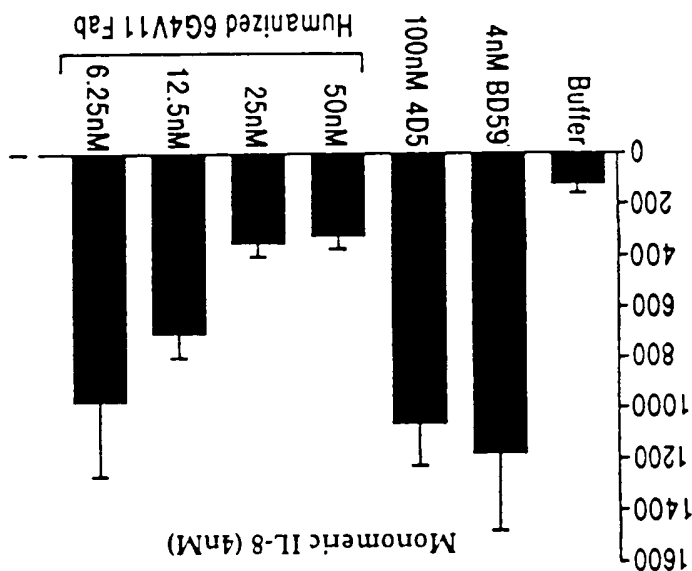
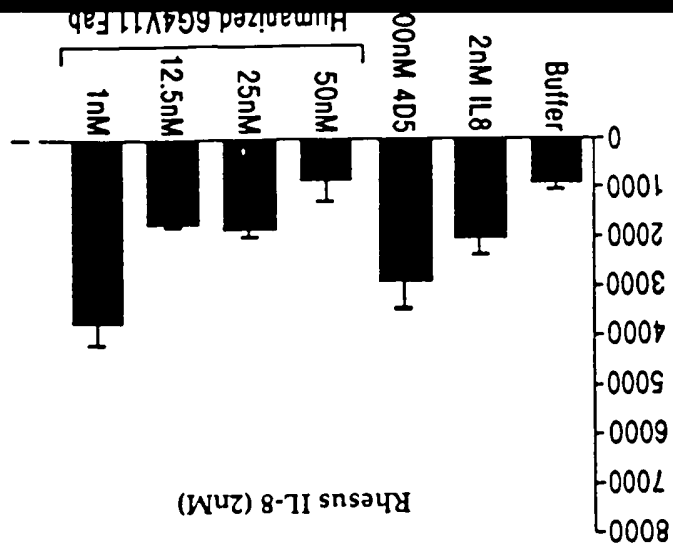


FIG. 30C

IC50~22nM



Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11 Light Chain

MKKNIAFLLASMEVFSIATNAYADIQMTQSPSSLSASVGDRVTITCRSSQSLVHGIGNTY
LHWYQQKPGKAPKLLIKVSNRFSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCSQST
HVLTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG
EC (See ID NO: 51)

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11 Heavy Chain

MKKNIAFLLASMEVFSIATNAYAEVOLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMH
WVRQAPGKLEWVGVIDPSNGETTYNQKFKGRFTLSRDNSKNTAYLQMNLSLRAEDTAVYY
CARGDYRYNGDWFEFDVWGQTLTVSSASTKGPVFPLAPSSKSTSGGTALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTK
VDKKVEPKSCDKTHT (See ID NO: 52)

Amino Acid Sequence of the peptide linker and M13 Phage Coat (gene-III)

SGGSGSGDFDYEKMANANKGAMTENADENALQSDAKGLDSVATDYGAIDGFIGDVS
GLANGNGATGDFAGSSNSQMAQVGDGDN SPLMNNFRQYLPSLPQSVCECRPFVFSAGKPY
EFSIDCDKINLFRGVFAFLLYVATFMVVFSTFANILRNKES (See ID NO: 53)

FIG. 31A

1 ATGAAAAGA ATATCCGATT TCTTCTGCA TCTATGTTG TTTTCTAT TGCTACAAC
-23 M K K N I A F L L A S M F V F S I A T N
61 GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCC TGTCGCCCTC TGTCGCCCTC
-3 A Y A D I Q M T Q S P S S L S A S V G D
121 AGGCTACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TAACACGTAT
18 R V T I T C R S S Q S L V H G I G N T Y
181 TTACACTGGT ATCAACAGAA ACCAGGAAA GCTCCGAAAC TACTGATTTA CAAGTATCC
AATGTAGCA TAGTTGTTCTT TGGTCTCTT CGAGGCTTTG ATGACTTAAT GTTTCATAGG
38 L H W Y Q Q K P G K A P K L L I Y K V S
241 AATGATTCT CTGAGTCCC TTCTGCTTC TCTGATCCG GTTCTGGAC GATTTCAC
58 N R F S G V P S R F S G S G S G T D F T
301 CTGACCATCA GCAGTCTCA GCCAAGAC TTCGAACTT ATTACTGTTT ACAGACTAT
78 L T I S S L Q P E D F A T Y Y C S Q S T
361 CATGTCCCG TCACGTTTG ACAGGTAC AAGTGGAGA TCAACGAAC TGTGCTGA
98 H V P L T F G Q G T K V E I K R T V A A
421 CCATCTGTCT TCATCTTCCC GCATCTGAT GAGCAATTGA AATCTGGAAC TGTCTGTT
118 P S V F I F P P S D E Q L K S G T A S V
481 GTGTGCTGC TGAATACTT CTATCCAGA GAGGCCAAG TACAGTGAA GTTGATAAC
138 V C L T N N F Y P R E A K V Q W K V D N
541 GCCCTCCAAT CCGTAACTC CCAGGAGAT GTACAGAGC AGCAGACA GAGCAGAC
158 A L Q S G N S Q E S V T E Q D S K D S T
601 TACAGCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACAGAAAACA CAAGTCTAC
178 Y S L S S T L T L S K A D Y E K H K V Y
661 GCCTGCGAAG TCACCCATCA GGCCTGAGC TCGCCCGTCA CAAGAGCTT CAACAGGGA
CGGACGCTTC AGTGGGTAGT CCGGAGCTCG AGCGGAGT GTTCTCGAA GTTGTCCCT
198 A C E V T H Q G L S S P V T K S F N R G
721 GAGTGTAAAG CTGATCTCTT ACCCGGAGC CATCGTGCC CTAGTACGA ACTAGTCTGA
CTCACAATTG GACTAGGAGA TGCGGCTTC GTAGCACCG GATCATGCGT TGATCAGCAT

218 E C O (56 10 10:51)

FIG. 31B

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V19 Light Chain

MKKNIAFLASMEVFSIATNAYADIQTQSPSSLSASVGDRVTTTCRSSQSLVHGIGNTY
LHWYQQKPGKAPKLLIKVSNRFSGVPSRFSGSGGTDFTLTISLQPEDFATYYCSQST
HVPLTEGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRG
EC (SEQ ID NO: 51)

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V19 Heavy Chain

MKKNIAFLLASMEVFSIATNAYAEVQLVESGGGLVQPGGSLRLSCAASGYSFSSHYMH
WVKQAPGKGLEWVGYPDPSNGETTYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYY
CARGDYRYNGDWFEDVWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTK
VDKKEPKSCDKHTT (SEQ ID NO: 55)

FIG. 31C

FIG. 32



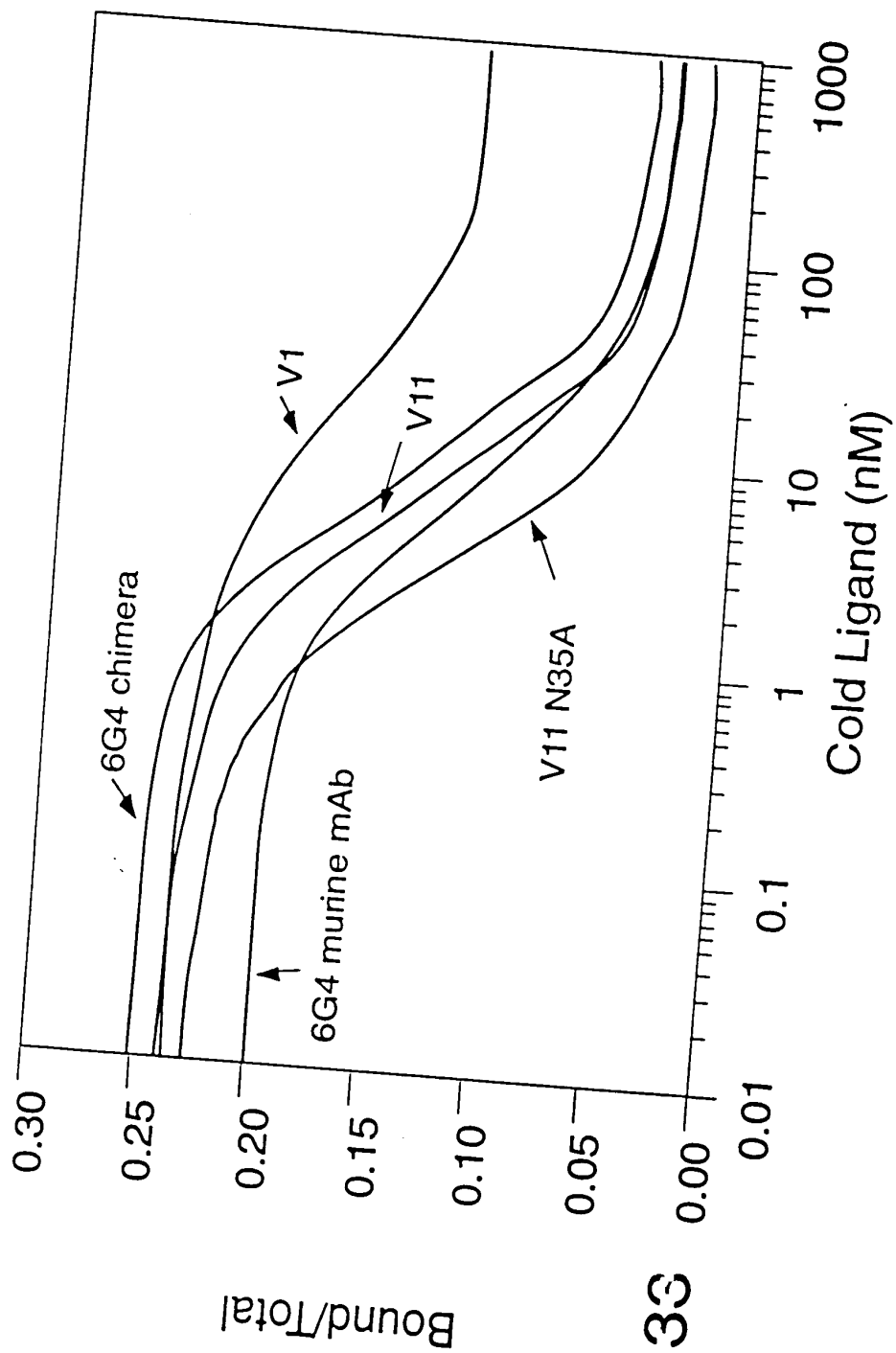
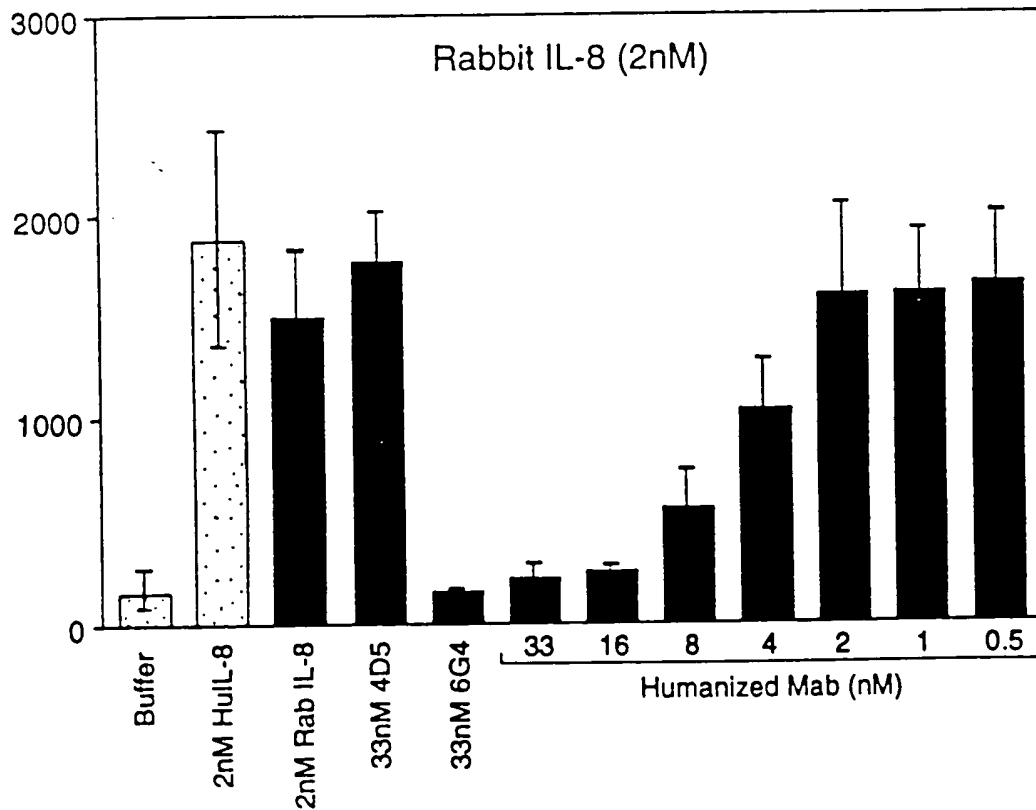
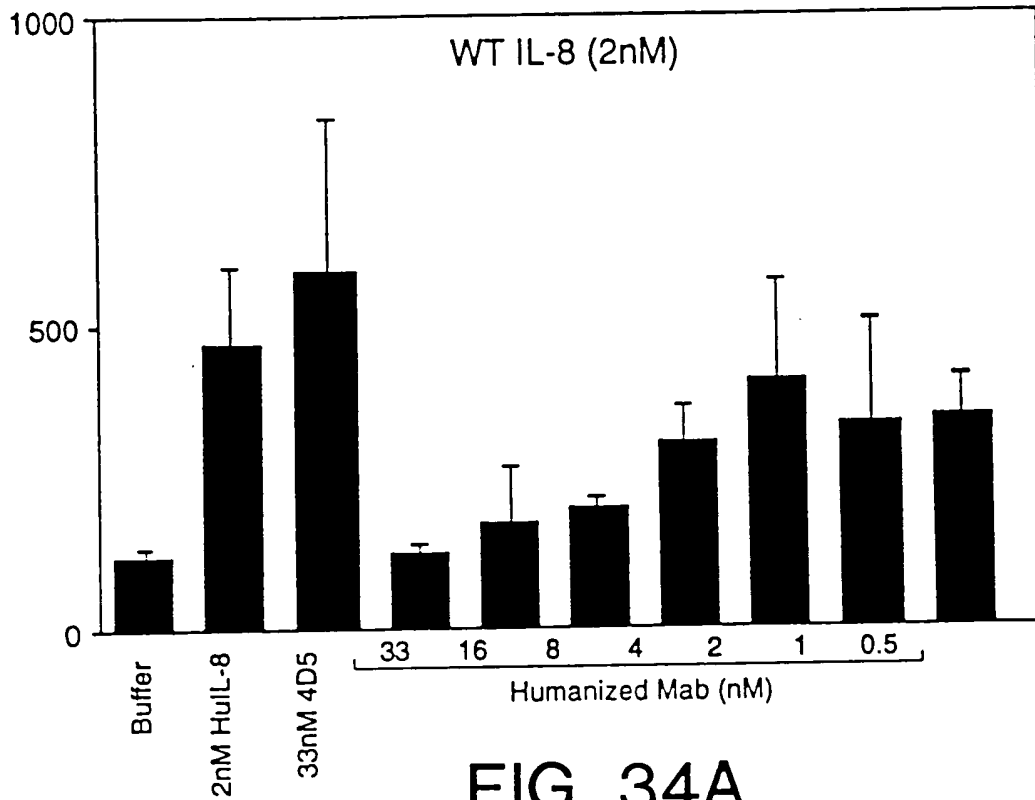


FIG. 33



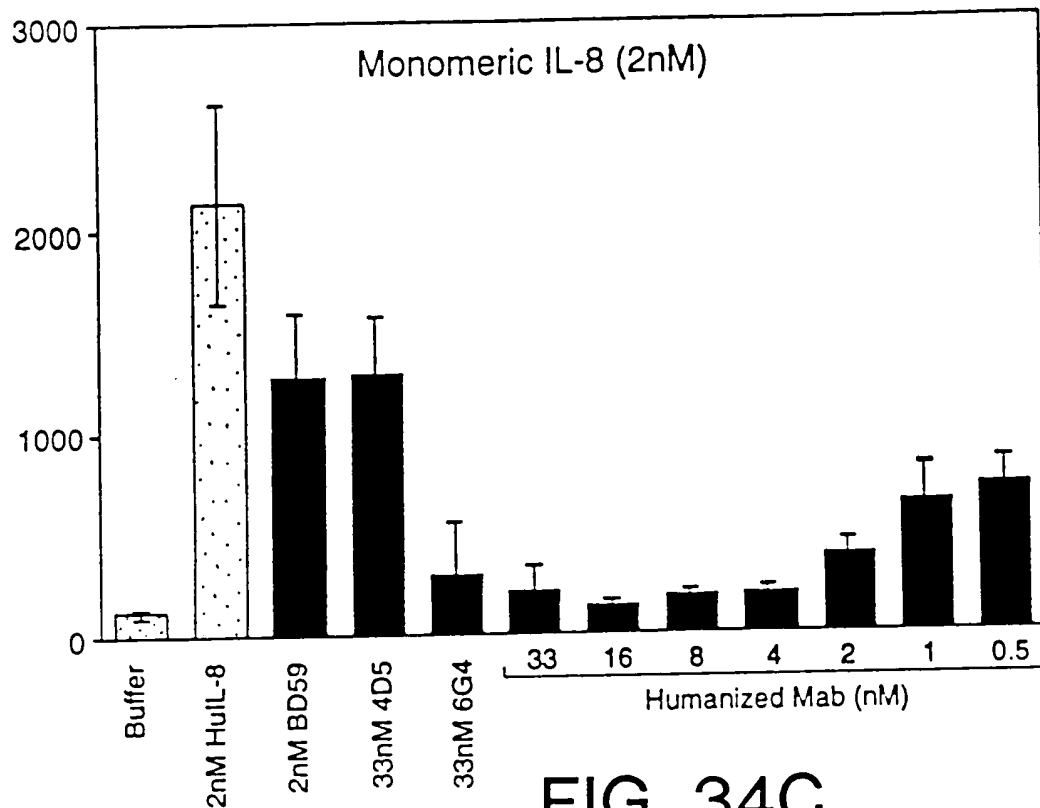


FIG. 34C

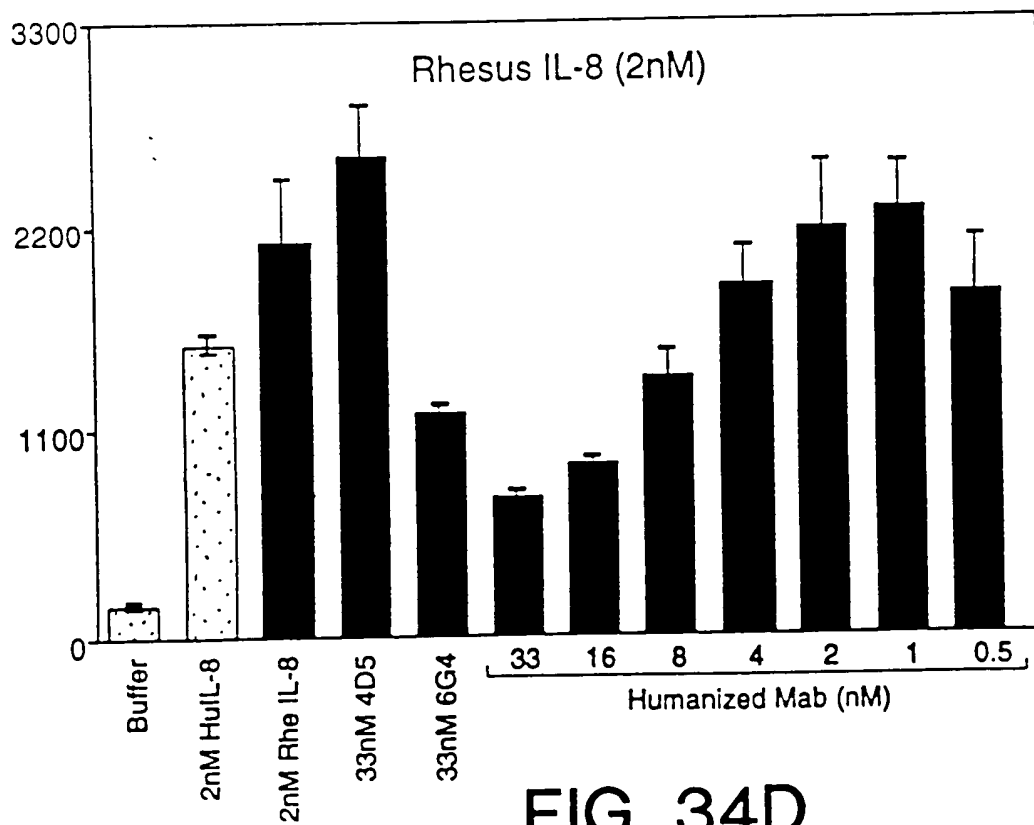


FIG. 34D

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11N35A Light Chain

MKKNIAFLASMFVFSIATNAYADIQMTQSPSSLSASVGDRTTITCRSSQSLVHGIGATY
LHWYQQKPGKAPKLLIYKVSNRFSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCSQST
HVPLTFGGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG
EC (SEQ ID NO: 56)

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11N35A Heavy Chain

MKKNIAFLASMFVFSIATNAYAEVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMH
WVRQAPGKGLEWVGYYIDPSNGETTYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYY
CARGDYRYNGDWFFDVWGQGLTVTVSSASTKGPVFFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTK
VDKKVEPKSCDKTHT (SEQ ID NO: 57)

Amino Acid Sequence of the putative Pepsin Cleavage Site and GCN4 Leucine Zipper

CPPCPAPELLGGRMKQLEDKVEELLSKNYHLENEVARLLKKLVGER (SEQ ID NO: 57)

FIG. 35

1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAC
 TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
 -23 M K K N I A F L L A S M F V F S I A T N
 61 GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCGGCCTC TGTGGGCGAT
 CGTATGCGAC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA
 -3 A Y A D I Q M T Q S P S S L S A S V G D
 121 AGGGTCACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TGCTACGTAT
 TCCCAGTGGT AGTGGACGTC CAGTTCAGTT TCGAATCATG TACCATATCC ACGATGCATA
 18 R V T I T C R S S O S L V H G I G A T Y
 181 TTACACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC
 AATGTGACCA TAGTTGTCTT TGGTCCTTTT CGAGGCTTTG ATGACTAAAT GTTTCATAGG
 38 L H W Y Q Q K P G K A P K L L I Y K V S
 241 AATCGATTCT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT
 TTAGCTAAGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG CCTAAAGTGA
 58 N R F S G V P S R F S G S G S G T D F T
 301 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC ACAGAGTACT
 GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAAG TGTCTCATGA
 78 L T I S S L Q P E D F A T Y Y C S O S T
 361 CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA
 GTACAGGGCG AGTGCAAACC TGTCCCATGG TTCCACCTCT AGTTTGCTTG ACACCGACGT
 98 H V P L T F G Q G T K V E I K R T V A A
 421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT
 GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA
 118 P S V F I F P P S D E Q L K S G T A S V
 481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
 CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG
 138 V C L L N N F Y P R E A K V Q W K V D N
 541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
 CGGGAGGTTA GCCCATTGAG GGTCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCTGTT
 158 A L Q S G N S Q E S V T E Q D S K D S T
 601 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
 ATGTCCGAGT CGTCGTGGGA CTGCGACTCG TTTCTGTCTGA TGCTCTTTGT GTTTCAGATG
 178 Y S L S S T L T L S K A D Y E K H K V Y
 661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
 CGGACGCTTC AGTGGGTAGT CCCGACTCG AGCGGGCAGT GTTCTCGAA GTTGTCCCTT
 198 A C E V T H Q G L S S P V T K S F N R G
 721 GAGTGTTAAG CTGATCCTCT ACGCCGGACG CATCGTGGCC CTAGTACGCA ACTAGTCGTA (SEQ ID NO: 58)
 CTCACAATTC GACTAGGAGA TGCGGCCTGC GTAGCACCAG GATCATGCGT TGATCAGCAT
 218 E C O (SEQ ID NO: 56)

FIG. 36

781 AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT TCTTCTTGCA
TTTTCCCATG GATCTCCAAC TCCACTAAAA TACTTTTTCT TATAGCGTAA AGAAGAACGT
-1 M K K N I A F L L A

841 TCTATGTTTCG TTTTTTCTAT TGCTACAAAC GCGTACGCTG AGGTTCAGCT AGTGCAGTCT
AGATACAAGC AAAAAAGATA ACGATGTTTG CGCATGCGAC TCCAAGTCGA TCACGTCAGA
-11 S M F V F S I A T N A Y A E V Q L V Q S

901 GCGGGTGGCC TGGTGCAGCC AGGGGGCTCA CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC
CGGCCACCGG ACCACGTCGG TCCCCCGAGT GAGGCAAACA GGACACGTCG AAGACCGATG
8 G G G L V Q P G G S L R L S C A A S G Y

961 TCCTTCTCGA GTCACTATAT GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG
AGGAAGAGCT CAGTGATATA CGTGACCCAG GCAGTCCGGG GCCCATTTCCG GGACCTTACC
28 S F S S H Y M H W V R Q A P G K G L E W

1021 GTTGGATATA TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT
CAACCTATAT AACTAGGAAG GTTACCACTT TGATGCATAT TAGTTTTCAA GTTCCCGGCA
48 V G Y I D P S N G E T T Y N O K F K G R

1081 TTCACCTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA CAGCCTGCGT
AAGTGAAATA GAGCGCTGTT GAGGTTTTTG TGTCGTATGG ACGTCTACTT GTCGGACGCA
68 F T L S R D N S K N T A Y L Q M N S L R

1141 GCTGAGGACA CTGCCGTCTA TTACTGTGCA AGAGGGGATT ATCGCTACAA TGGTGACTGG
CGACTCCTGT GACGGCAGAT AATGACACGT TCTCCCCTAA TAGCGATGTT ACCACTGACC
88 A E D T A V Y Y C A R G D Y R Y N G D W

1201 TTCTTCGACG TCTGGGGTCA AGGAACCCTG GTCACCGTCT CCTCGGCCTC CACCAAGGGC
AAGAAGCTGC AGACCCAGT TCCTTGGGAC CAGTGCGAGA GGAGCCGGAG GTGGTTCCCG
108 F F D V W G Q G T L V T V S S A S T K G

1261 CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG
GGTAGCCAGA AGGGGGACCG TGGGAGGAGG TTCTCGTGGA GACCCCGTG TCGCCGGGAC
128 P S V F P L A P S S K S T S G G T A A L

1321 GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC
CCGACGGACC AGTTCTGAT GAAGGGGCTT GGCCACTGCC ACAGCACCTT GAGTCCGCGG
148 G C L V K D Y F P E P V T V S W N S G A

1381 CTGACCAGCG GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC
GACTGGTTCG CGCACGTGTG GAAGGGCCGA CAGGATGTCA GGAGTCCTGA GATGAGGGAG
168 L T S G V H T F P A V L Q S S G L Y S L

1441 AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG
TCGTGCGACC ACTGGCACGG GAGGTCGTCG AACCCGTGGG TCTGGATGTA GACGTTGCAC
188 S S V V T V P S S S L G T Q T Y I C N V

1501 AATCACAAGC CCAGCAACAC CAAGGTCGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA
TTAGTGTTTCG GGTGCTTGTG GTTCCAGCTG TTCTTTCAAC TCGGGTTTAG AACACTGTTT
208 N H K P S N T K V D K K V E P K S C D K

1561 ACTCACACAT GCCCGCCGTG CCCAGCACCA GAACTGCTGG GCGGCCGCAT GAAACAGCTA
TGAGTGTTGA CGGGCGGCAC GGGTCGTGGT CTTGACGACC CGCCGGCGTA CTTTGTCGAT
228 T H T C P P C P A P E L L G G R M K Q L

FIG. 37A

1621 GAGGACAAGG TCGAAGAGCT ACTCTCCAAG AACTACCACC TAGAGAATGA AGTGGCAAGA
CTCCTGTTCC AGCTTCTCGA TGAGAGGTTC TTGATGGTGG ATCTCTTACT TCACCGTTCT
248 E D K V E E L L S K N Y H L E N E V A R

1681 CTCAAAAAGC TTGTCGGGGA GCGCTAA (SEQ ID NO: 59)
GAGTTTTTCG AACAGCCCCT CGCGATT
268 L K K L V G E R O (SEQ ID NO: 60)

FIG. 37B

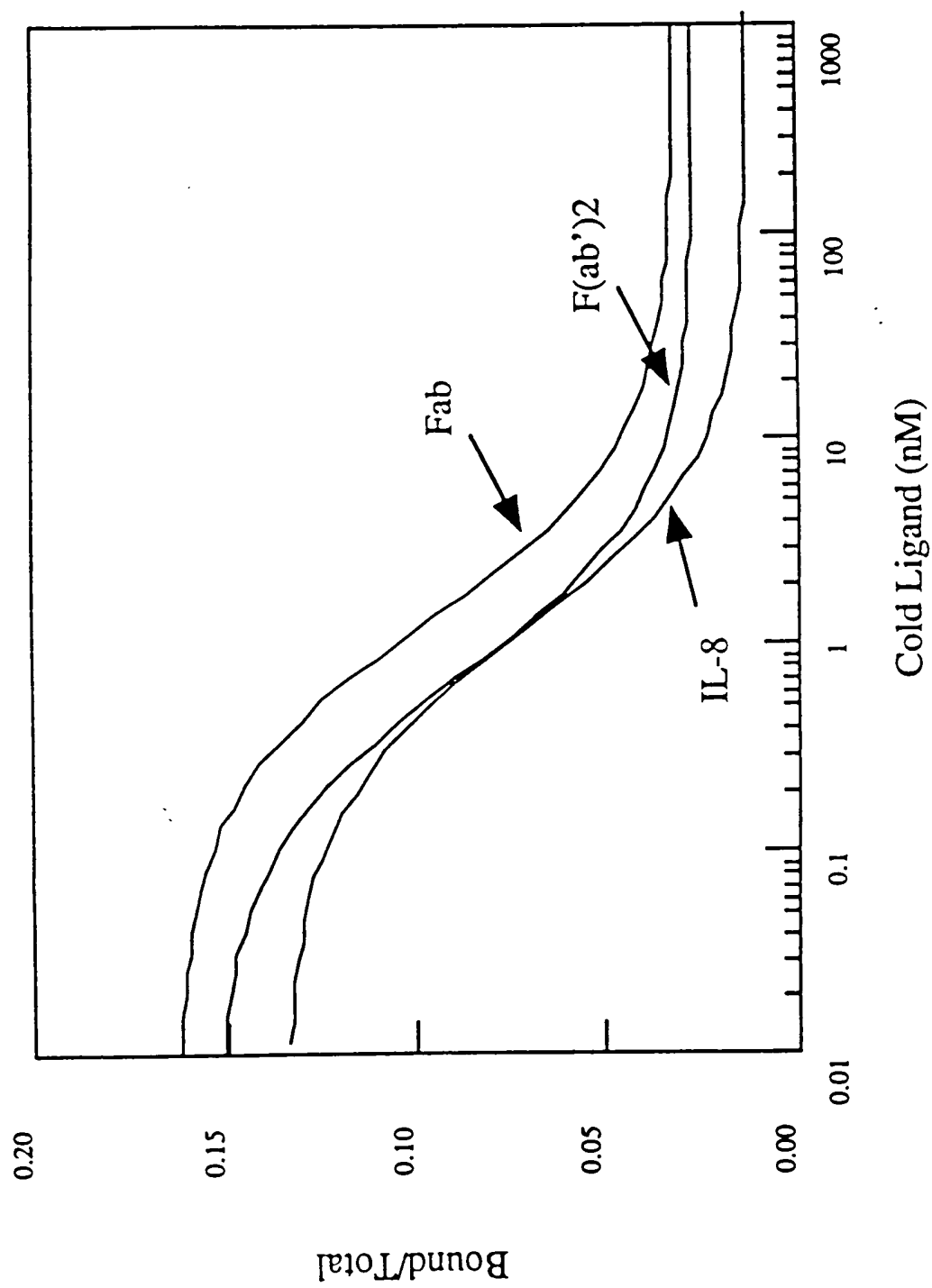


FIG. 38

FIG. 39

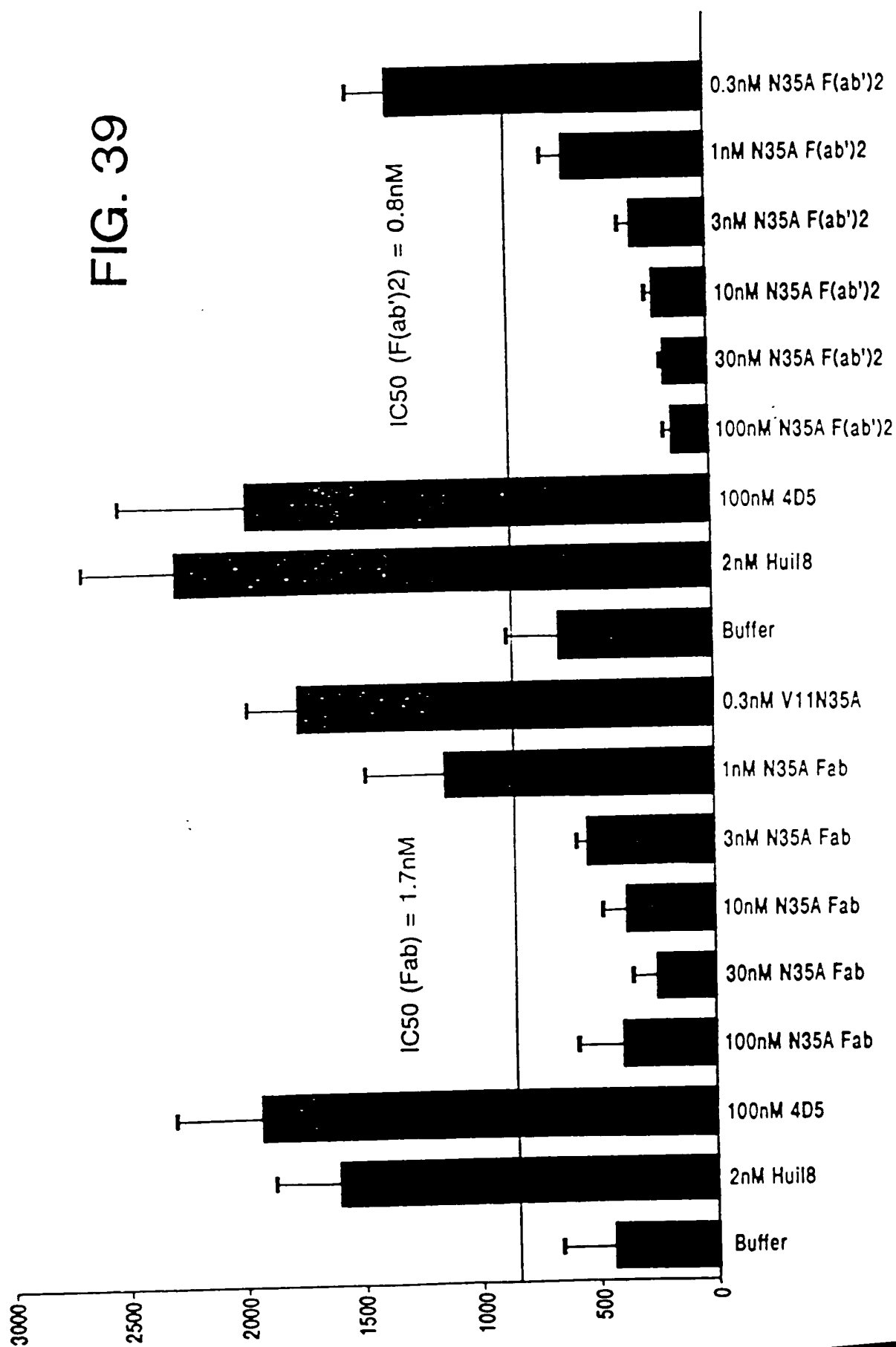
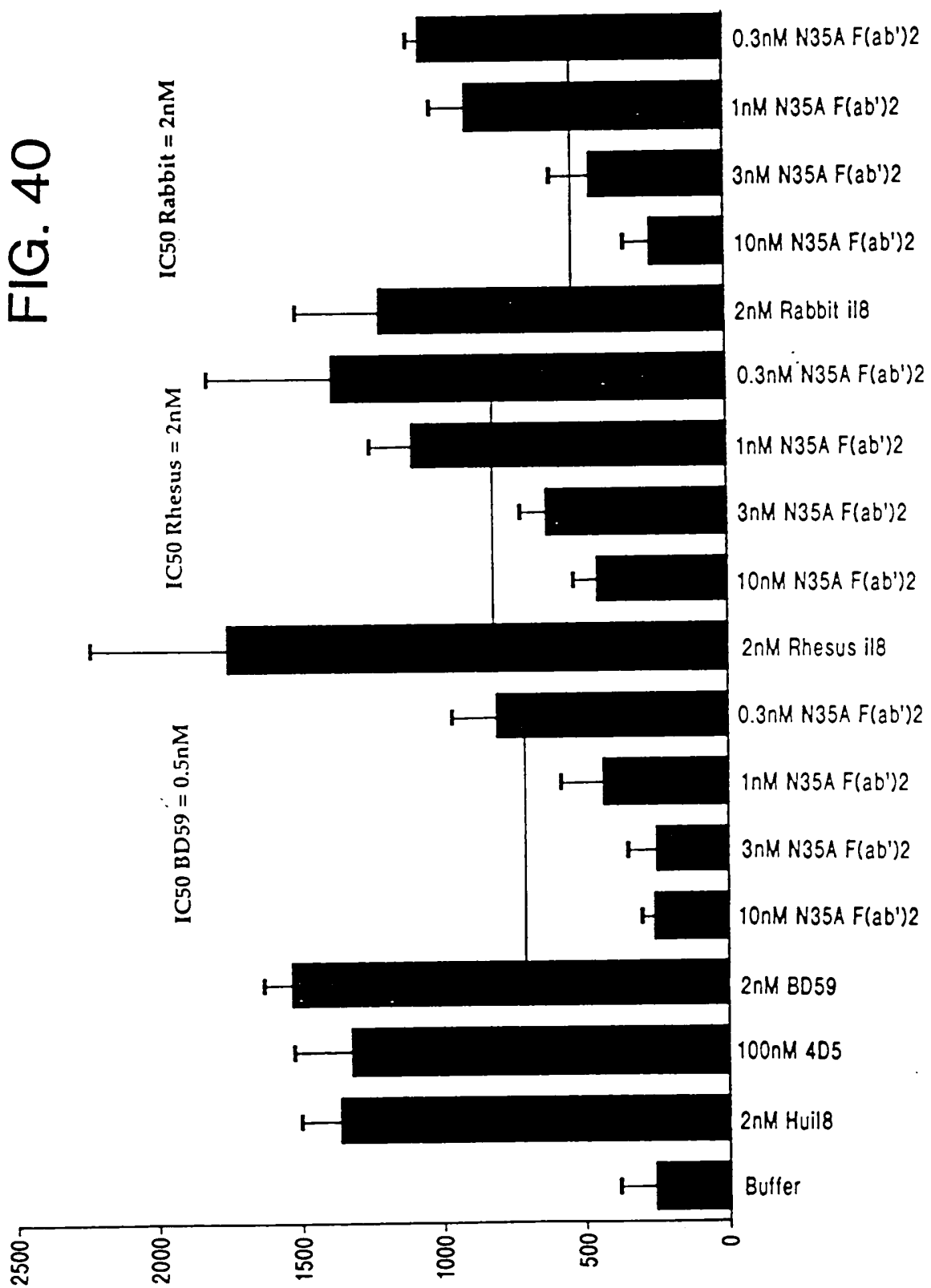


FIG. 40



ecoRI pflMI
apoI bslI

1 GAATTCAACT TCTCCATACT TTGGATAAGG AANTACAGAC ATGAANAATC TCATTGCTGA GTTGTATTAT MAGCTTGCCC AAAAGAAGA AGACTCGAAT CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGCTG TACTTTTTAG AGTACGACT CAACAATAMA TTCGAACGGG TTTTCTCTCT TCTCAGCTTA

bspMI
hinPI
hhaI/cfoI
mstII aluI
avIII/fspI hindIII

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG CTTGACACAC CGGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTAC TGGTTGTCGC CAACTAACCTA GTCCATCTCC

rsal
hinPI
hhaI/cfoI mnlI
haeII csp6I

201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCCTGA CGACGATACG GAGCTGCTGC CGCATTTACGT AAAGAGTTA TTGAAGCATC CTCGTCAGTA CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

pleI
mboII taqI
earI/ksp632I
mboII hinfI

aluI
hindIII
tru9I
ddeI
bsrDI
nlaIII
mslI
maeIII bsrDI
mslI
maeIII bsrDI
acuI
hinPI
hhaI/cfoI
nspBII
bclI[dam-] mnlI

sau3AI
mboI/ndeII[dam-]
dpnI[dam+]
dpnII[dam-]

thaI
fnuDII/mvni
fnu4HI
bsoFI
bbvI
fnu4HI bstUI snaBI
bsoFI bsh1236I
bbvI hinPI bsaAI
aluI hhaI/cfoI

maeII
maeII
foki
sfaNI

haeIII/pali
mcRI
eagI/xmaIII/eclXI
caeI
cfri
bsiEI
maeIII bsmAI
maeIII apoI banII

tru9I
pvuII
mspBII

aluI
trun9I
mseI

ecori
bspl286
imaI
maei
bfai
taqi

hsaI
hgiJII
hglAI/aspHI
ecl136II

101 AAAAGTTAAT CTTTTCACCA GCTGTCATAA AGTTGTACG GCCGAGACTT ATAGTCGCTT TCTTTTTATT TTTTAACTGA TTTGTAACCTA GAATTCGAGC TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACANAAATMA AAAATTACAT AAACATTGAT CTTAAGCTCG

FIG. 41A

scrFI
 nciI
 mspI
 hpaII
 dsav
 xmaI/pspAI
 smaI
 scrFI
 nciI
 dsav
 cauII
 bsaJI
 xhoI
 mnlI
 sau3AI taqI
 rsaI mboI/ndeII[dam-]
 csp6I dpnI[dam+]
 nlaIV nlaIV paeR7I
 kpnI cauII dpnII[dam-]
 hgiCI bstYI/xhoII
 bani bsaJI alwI[dam-]
 asp718 bamHI avaI hphI
 acc65I alwI[dam-] mnlI mnlI
 401 TCGGTACCCG GGGATCCTCT CGAGGTTGAG GTGATTTTAT GAAAGAAGAT ATCGCATTTT TTTCTTGGATC TATGTTTCGTT TTTTCTATTG CTACAAACGC
 AGCCATGGGC CCCTAGGAGA GCTCCNACTC CACTAAATA CTTTTCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA AAAAGATAAC GATGTTTGGC
 M K K N I A F L L A S M F V F S I A T N A
 a mutation was found that inactivated the mluI site. The penultimate nucleotide was changed fr G toT ^
 -23
 sstI
 sacI
 hgiJII
 hgiAI/aspHI
 ecll36II
 bspl286
 bsiHKAI
 bsmFI bmyI
 bsmFI avaI aluI
 tthlIII/aspI banII
 acil
 TCCGCCCTCTG TGGGGCGATAG GGTCACCATC ACCTGCAGGT CAAGTCAAAG CTTAGTACAT
 AGCGGGAGAC ACCCGGTATC CCAGTGGTAG TGGACGTCCA GTTCAGTTTC GAATCATGTA
 S A S V G D R V T I T C R S S Q S L V H
 bspMI
 scfI
 pstI
 hphI
 maeIII
 bstEII hphI.bsgI
 sse8387I
 bspMI
 aluI
 rsal
 ddeI nlaIII
 01 ATACGCTGAT ATCCAGATGA CCCAGTCCCC GAGCTCCCTG
 -2 Y A D I Q M T Q S P S S L S A S V G D R V T I T C R S S Q S L V H

-23

FIG. 41B

601	GGTATAGGTG	CTACGTATTT	ACACTGGTAT	CAACAGAAAC	CAGGAAAGC	TCCGAAACTA	CTGATTACAA	AAGTATCCAA	TCGATTCTCT	GGAGTCCCTT
	CCATATCCAC	GATGCATANA	TGTGCTTTTG	GTCCTTTTCG	AGGCTTTTGT	GACTAATGT	TTCATAGGTT	AGCTAAGAGA	CCTCAGGGAA	
32	G I G A	T Y L H	W Y Q Q	K P G K	A P K L	L I Y K	V S N R	F S G V	P S	

701	CTCGCTTCTC	TGGATCCGGT	TCTGGGACGG	ATTCACTCT	GACCATCAGC	AGTCTGCAGC	CAGAGACTT	CGCAACTTAT	TACTGTTTAC	AGAGTACTCA
	GAGCGAAGAG	ACCTAGGCCA	AGACCTTGCC	TAAAGTGAGA	CTGGTAGTCG	TACAGAGTCG	GTCTTCTGAA	CGGTTGAATA	ATGACAAGTG	TCTCATGAGT
66	R F S G	S G S G	T D F T	L T I S	S L Q P	E D F A	T Y Y C	S Q S T	H	

1	TCCTCCGCTC	ACGTTTGAC	AGGTACCAA	GGTGGAGATC	AAACGNACTG	TGGCTGCACC	ATCTGTCTTC	ATCTTCCCGC	CATCTGATGA	GCAGTTGAAA
	ACAGGGCGAG	TGCAAACTG	TCCCATGGTT	CCACCTCTAG	TTTGCTTGAC	ACCGACGTGG	TAGACAGAG	TAGAAGGGCG	GTAGACTACT	CGTCAACTTT
9	V P L T	F G Q G	T K V E	I K R	T V A A	P S V F	I F P P	S D E Q	L K	

FIG. 41C

[illegible]

FIG. 41D

1201 AGTACGCMAC TAGTCGTAMA AAGGGTATCT AGAGGTTGAG GTGATTTTAT GAAAAAGAAAT ATCGCATTTT TCCTTGCATC TATGTTTCGTT TTTTCTATTG
 TCATGCGGTG ATCAGCATTT TTCCCATAGA TCCCCACTC CACTAAATA CTTTCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA AAAAGATAAC
 M K K N I A F L L A S M F V F S I A

-23

1301 CTACAAACGC GTACGCTGAG GTTCAGCTAG TGCAGTCTGG CGGTGGCTG GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT CTGGCTACTC
 GATGTTTGG CATGCGACTC CAAGTCGATC ACGTACAGCC GCCACCGAC CACGTGGTC CCCCAGTCA GGCANACAGG ACACGTGAA GACCGATGAG
 -5 T N A Y A E V Q L V Q S G G L V Q P G G S L R L S C A S G Y S

FIG. 41E

pleI
 hinfI
 taqI
 xhoI
 pacR7I
 avai maeIII
 sau96I
 avaiI
 asuI
 nlaIV
 sau96I
 sau96I
 nlaIV
 haeIII/pali
 asuI
 ecoO109I/draII
 haeIII/pali
 TCGAGGCCCG GGTAAAGGCC TGGMATGGGT TGGATATATT GATCCTTCCA ATGGTGAAAC TACGTATAAT
 GAAGAGCTCA GTGATATACG TGACCCAGGC AGTCCGGGGC CCATTCCCGG ACCTTACCCA ACCTATATAA CTAGGAAGGT TACCACCTTG ATGCATATTA
 29 F S S H Y M H W V R Q A P G G K G L E W V G Y I D P S N G E T T Y N
 thai
 fnuDII/mvni
 bstUI
 haeIII/pali
 sau96I
 asuI
 nruI
 CGCGACNACT CCNAAACAC AGCATACTG CAGATGAACA GCCTGCGTGC TGAGGACACT GCCGTCTATT
 CACTTTATCT CACTTATCT GTGAAATAGA GCGCTGTTGA GGTTTTGTG TCGTATGGAC GTCTACTGT CGGACGCACG ACTCCTGTGA CGGCAGATAA
 501 CAAAAGTTCA AGGCGCGTTT
 G T T T T C A G T T C C C G G C A A A
 62 Q K F K G R F T L S R D N S K N T A Y L Q M N S L R A E D T A V Y Y
 sau96I
 haeIII/pali
 sau96I
 nlaIV
 hgiJII
 bsp1286
 bsp120I
 bmyI
 banII
 asuI
 apaI
 styI asuI
 bsaJI
 mnlI
 haeIII/pali
 ecoO109I/draII
 ACTGTGCAAG AGGGGATTAT CGCTACAATG GTGACTGGTT CTTGACGCTG TGGGGTCAAG GMACCCTGTT CACCGTCTCC TCGGCCTCCA CCAAGGGCCC
 TGACACGTTT TCCCTTAATA CGGATGTTAC CACTGACCAA GAAGCTGCAG ACCCCAGTTC CTTGGGACCA GTGGCAGAGG AGCCGAGGT GGTTCCTCCGG
 6 C A R G D Y R Y N G D W F F D V W G Q G T L V T V S S A S T K G P
 seq right is from p6G425chlm2.fab2

FIG. 41E

[illegible]

FIG. 41G

fnu4HI
 bsoFI
 hacIII/pali
 mcrI
 eagI/xmaIII/ecI XI
 eaeI
 cfrI
 .bsiEI
 notI
 fnu4HI
 bsoFI nlaIII
 acII acII
 cac8I
 nlaIII
 nspI
 nspHI acII bmyI
 bsp1286
 2001 TCACACATGC CCGCCGTGCC CAGCACCAGA ACTGCTGGC GCGCGCATGA MACAGCTAGA GGACAAGGTC GAAGAGCTAC TCTCCAAGAA CTACCACCTA
 AGTGTGTACG GCGGCGACGG GTCGTGGTCT TGACGACCCG CCGCGGTACT TTGTCGATCT CCGTGTCCAG CTCTCGATG AGAGGTTCTT GATGGTGGAT
 229 H T C P P C P A P E L L G G R M K Q L E D K V E E L L S K N Y H L
 ~junction between antibody and leucine zipper
 phi
 ddeI nlaIII
 celII/espI
 blpI/bpull02I
 hinPI nspI
 hhaI/cfoI
 haeII nspHI
 eco47III cac8I
 pleI aluI
 hinFI hindIII
 2101 GAGAATGAG TGGCMAGCT CAAAAGCTT GTCGGGGAGC GCTAAGCATG CGACGGCCCT AGAGTCCCTA ACCTCGGTT GCGCGCGGGC GTTTTTTATT
 CTCTTACTC ACCGTTCTGA GTTTTTCGAA CAGCCCTCTG CGATTCTGAC GCTGCCGGA TCTCAGGAT TCGGAGCCAA CCGCGCGCCG CAAAAAATAA
 262 E N E V A R L K K L V G E R O (5' to 3')
 tru9I
 msel
 hpaI nlaIII
 hincII/hindII aluI
 2201 GTTAACATCAT GTTTGACAGC TTATCATCGA TAAGCTTTAA TGCGGTAGTT TATCAGAGTT AAATTGCTAA CGCAGTCAGG CACCGTGTAT GAAATCTAAC
 CAATTGAGTA CAAACTGTGC AATAGTAGCT ATTGCAATT ACGCCATCAA ATAGTGTCAA TTTAACGATT GGTTCAGTCC GTGGCACATA CTTTAGATTG

FIG. 41H

[illegible]

FIG. 41I

[illegible]

FIG. 41J

[illegible]

[illegible]

FIG. 41L

3501 CTAACGGATT CACCACTCCA AGAATTGGAG CCAATCAATT CTTGCGGAGA ACTGTGAATG CGCAACCCAA CCTTGGCAG AACATATCCA TCGCGTCCGC
GATTGCCTAA GTGGTGAGGT TCTTAACCTC GGTAGTTAA GMAAGCCTCT TGACACTTAC GCGTTGGTT GGGAAACCGTC TTGTATAGGT AGCGCAGCGC

3601 CATCTCCAGC AGCGCAGCG GCGCATCTC GGGCAGCGT GGGTCTCGC CACGGGTGCG CATGATCGTG CTCCTGTCGT TCAGGACCCG GCTAGGCTGG
GTAGAGGTCTG TCGGCGTGCG CCGGTAGAG CCCGTCCGA CCCAGGACCG GTGCCACCG GTACTAGCAC GAGGACAGCA ACTCTGGGC CGATCCGACC

FIG. 41M

sau3AI
 mboI/ndeII(dam-)
 mamI(dam-)
 dpuI(dam+)
 dpnII(dam-)
 bstYI/xhoII
 alwI(dam-)
 mspI
 hpaII
 mroI bsaBI(dam-)
 bspMII
 bspEI(dam-)
 bsaWI sfaNI
 accIII(dam-)
 TTATGTTCG GATCTGCATC GCAGGATGCT GCTGGCTACC
 AATACAAGGC CTAGACGTAG CGTCTACGA CGACCGATGG
 cac8I
 hinPI
 hhaI/cfoI
 bsh1236I haeII mslI
 bsh1236I haeII mslI
 TGGTAAAGTC TCGTAAAGTC TTTCCGTGTT
 ACCAGAAAGCC AAAGGCACAA AGCATTTCAG ACCTTTGGC CTTCACTGC GGGACGTGGT
 acII
 thaI
 fnuDII/mvni hinPI
 bstUI hhaI/cfoI
 bsh1236I haeII mslI
 TGGTAAAGTC TCGTAAAGTC TTTCCGTGTT
 ACCAGAAAGCC AAAGGCACAA AGCATTTCAG ACCTTTGGC CTTCACTGC GGGACGTGGT
 cac8I
 hinPI
 hhaI/cfoI
 tru9I haeII
 maeI eco47III
 CTGTGGNACA CCTACATCTG TATTAACGAA GCGCTGGCAT TGACCCCTGAG TGATTTTCT ACTGAGACTC ACTAAAGA GACCAGGGCG GCGTAGGTAT GCGGTCAAC AAATGGGAGT
 GACACCTTGT GGATGTAGAC ATAATTGCTT CCGGACCGTA ACTGGGACTC ACTGAGACTC ACTAAAGA GACCAGGGCG GCGTAGGTAT GCGGTCAAC AAATGGGAGT
 nspI
 scrFI
 nciI
 mspI
 hpaII
 bslI
 dsav nlaIII
 maeII
 cauII
 pspl406I maeIII nspHI
 CAACGTTCCA GTACCGGGC ATGTTTCATCA TCAGTAACCC
 GTATCGTGAG CATCTCTCT
 CATAGCACTC GTAGAGAGA GCAAGTAGC CATAGTAATG GGGGTACTTG TCTTTAAGGG
 nlaIII
 apoI
 bslI
 TTTACCCCTCA
 AAATGGGAGT

FIG. 41N

[illegible]

[illegible]

FIG. 41P

Restriction Enzyme	Sequence
4801	<p> scrFI mvaI mvaI ecoRII dsav dsav bstNI bstNI apyI[dcM+] bsaJI aluI mnlI hhaI/cfoI AGACTATAA AGATACCAGG CGTTTCCCC TGGAGCTCC CTCGTGGCT CTCCTGTTCC GACCCCTGCC CTTACCGGAT ACCTGTCCGC CTTTGGGCTG TCCTGATATT TCTATGGTCC GCAAGGGGG ACCITCGAGG GAGCAGCGA GAGGACNAGG CTGGGACGGC GAAATGGCCTA TGGACAGCGC </p>
4901	<p> scrFI mvaI mvaI ecoRII dsav dsav bstNI bstNI apyI[dcM+] bsaJI aluI mnlI hhaI/cfoI AGACTATAA AGATACCAGG CGTTTCCCC TGGAGCTCC CTCGTGGCT CTCCTGTTCC GACCCCTGCC CTTACCGGAT ACCTGTCCGC CTTTGGGCTG TCCTGATATT TCTATGGTCC GCAAGGGGG ACCITCGAGG GAGCAGCGA GAGGACNAGG CTGGGACGGC GAAATGGCCTA TGGACAGCGC </p>
001	<p> scrFI mvaI mvaI ecoRII dsav dsav bstNI bstNI apyI[dcM+] bsaJI aluI mnlI hhaI/cfoI AGACTATAA AGATACCAGG CGTTTCCCC TGGAGCTCC CTCGTGGCT CTCCTGTTCC GACCCCTGCC CTTACCGGAT ACCTGTCCGC CTTTGGGCTG TCCTGATATT TCTATGGTCC GCAAGGGGG ACCITCGAGG GAGCAGCGA GAGGACNAGG CTGGGACGGC GAAATGGCCTA TGGACAGCGC </p>
01	<p> scrFI mvaI mvaI ecoRII dsav dsav bstNI bstNI apyI[dcM+] bsaJI aluI mnlI hhaI/cfoI AGACTATAA AGATACCAGG CGTTTCCCC TGGAGCTCC CTCGTGGCT CTCCTGTTCC GACCCCTGCC CTTACCGGAT ACCTGTCCGC CTTTGGGCTG TCCTGATATT TCTATGGTCC GCAAGGGGG ACCITCGAGG GAGCAGCGA GAGGACNAGG CTGGGACGGC GAAATGGCCTA TGGACAGCGC </p>

FIG. 41Q

[illegible]

FIG. 41B

[illegible]

FIG. 41S

001 ATTCTCTTAC TGTCATGCCA TCCGTAAGAT GCTTTTCTGT GACTGGTGAG TACTCAACCA AGTCATTCTG AGAATAGTGT ATCGCGCGGAC CGAGTTGCTC
TAGAGAAATG ACAGTACGGT AGGCATTCTA CGAAAGACA CTGACCACCTC ATGAGTTGGT TCAGTATGAC TCTTATCACA TACGCCGCTG GCTCAACGAG

01 TTGCCCGCG TCAACACGGG ATATATACCGC GCCACATAGC AGAATCTTAA AGTGCTCAT CATTGGAAA CGTTCTTCGG GCGGAAACT CTCGAAGGATC
AACGGGCGC AGTTGTGCC TATTATGGCG CGGTGTATCG TCTTGAAATT TTCACGAGTA GTAACCTTTT GCAAGAAGCC CGCTTTTGA GAGTTCCTAG

01 TTACCGCTGT TGAGATCCAG TTCGATGTAA CCCACTCGTG CACCCAACTG ATCTTCAGCA TCTTTTACTT TCACCAGCGT TTCTGGGTGA GCNAAAACAG
AATGGCGACA ACTCTAGGTC AAGCTACATT GGTGAGCAC GTGGGTTGAC TAGAAGTCGT TAGAAGTCGT AGAAGTGA AGTGGTCCGA AAGACCCACT CGTTTTTGTG

6401	TTGTCTCATG	AGCGGATACA	TATTGTAATG	TATTTAGTAA	ATAAACAATA	TAGGGTTTCC	GCGCACATTT	CCCCGAAAAG	TGCCACCTGA	CGTCTAAGAA
	AACAGAGTAC	TGGCCATGCT	ATAAACTTAC	ATAAATCTTT	TTATTTGTTT	ATCCCCAAGG	CGCGTGTAAG	GGGGCTTTC	ACGGTGGACT	GCAGATTCTT

6501	ACCATTATTA	TCATGACATT	AACCTATATA	AATAGGCGTA	TCACGAGGCC	CTTTCGTCTT	CMA
	TGGTAATAAT	AGTACTGTAA	TTGGATATTT	TTATCCGCAT	AGTGCTCCGG	GAAAGCAGAA	GTT

nlaIII rcaI bspHI bsmAI bsrBI	hinPI thal fnuDII/mvnI bstUI bsh1236I aciI nlaIV hhaI/cfoI	maeII hinII/acyI ahaII/bsaHI aatII ddeI
---	---	--

nlaIII rcaI bspHI mseI	sau96I haeIII/palI asuI ecoO109I/draII mnlI bssSI bbsI	mboII bpuAI bbsI
---------------------------------	--	------------------------

(SEQ ID NO: 61)

FIG. 41U

```

>length: 6563

aatII(GACGTC): 1645 6489
acc65I(GGTACC): 403 823
accI(GTAKAC): 1093 1963 4449
accIII(TCCGGA): 3867[dam-]
acII(CCGC): 178 542 805 877 1340 1750 1826 2011 2039 2043 2182 2242 2384 2492 2501 2504
2628 2781 2784 2787 2906 2926 3005 3045 3094 3141 3226 3241 3309 3342 3367 3412
3436 3448 3490 3544 3597 3613 3619 3700 3838 3967 3970 3981 4139 4155 4210 4266
4351 4390 4400 4442 4467 4505 4518 4544 4561 4604 4611 4632 4723 4751 4878 4897
5018 5128 5263 5272 5634 5725 5916 5962 6083 6127 6204 6313 6412 6459
see hinI
acyI 1307 4678
afIIII(ACRYGT): 1788
ageI(ACCGGT): 1645 1813 2616 2637 2751 3408 6107 6489
ahaII/bsaHI(GRCGYC): 1645 1813 2616 2637 2751 3408 6107 6489
ahaIII/draI(TTTAAA): 5435 5454 6146
ahdI/eam1105I(GACNNNNNGTC): 346 5566
72 121 252 320 398 532 589 648 1126 1144 1167 1325 1386 1906 2054 2075 2126
2218 2233 2889 3292 4202 4259 4270 4319 4338 4619 4845 4935 4981 5238 5759 5859
5922
aluI(AGCT): 1831 4494 4992 6238
412 413 712 713 1171 1471 2578 2579 3300 3870 5245 5319 5331 5416 5429 5893
6196 6214
alw44I/snoI(GTGCAC): 1117 1385 5089
alwI[dam-](GGATC): 1695
6196 6214
alwNI[dcm-](CAGNNNCTG): 1117 1385 5089
apaI(GGGCCC): 1695
apaLI/snoI(GTGCAC): 1831 4494 4992 6238
apoI(RAATY): 1 391 4093
apyI[dcm+](CCWGG): 640 999 1347 1357 1449 1665 1713 1755 1764 2333 3262 3645 4705 4826 4839
aseI/asnI/vspI(ATTAAAT): 5742
asnI see aseI
asp700(GAANNNTTC): 905 930 4234 6166
asp718(GGTACC): 403 823
asphi see hglAI
aspi see tth111I
asuI(GGNCC): 1119 1195 1425 1434 1446 1512 1695 1696 1752 2155 2375 2727 3002 3090 3339 3463

```

FIG. 41V

Stop Template Primer

SL.97.2 5' CAT GGT ATA GGT TAA ACT TAT TTA CAC 3' (SEQ ID NO: 63)

NNS Randomization Primer

SL.97.3 5' CAT GGT ATA GGT NNS ACT TAT TTA CAC 3' (SEQ ID NO: 64)

FIG. 42

Randomization of Position N35 of Variable Light Chain CDR-1
Amino Acid Frequency

Phage Display (NNS Codon Library) Sort #3

Amino Acid	Frequency	% Total	IC50 (nM)
Asparagine (wt)	1	5.6	4.9
Glycine	6	16.6	3.1
Aspartic Acid	3	16.6	3.1
Glutamic Acid	4	22.2	0.1
Alanine	2	5.6	0.2
Lysine	1	5.6	ND
Serine	1	1.9	ND

FIG. 43A

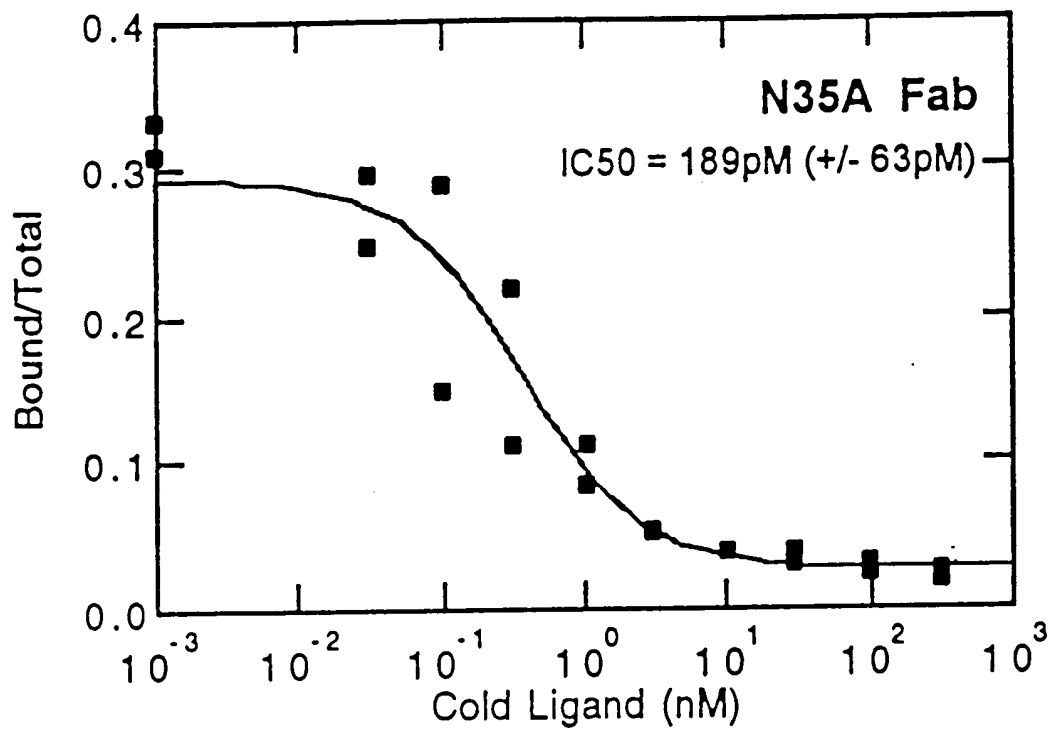


Fig 43B

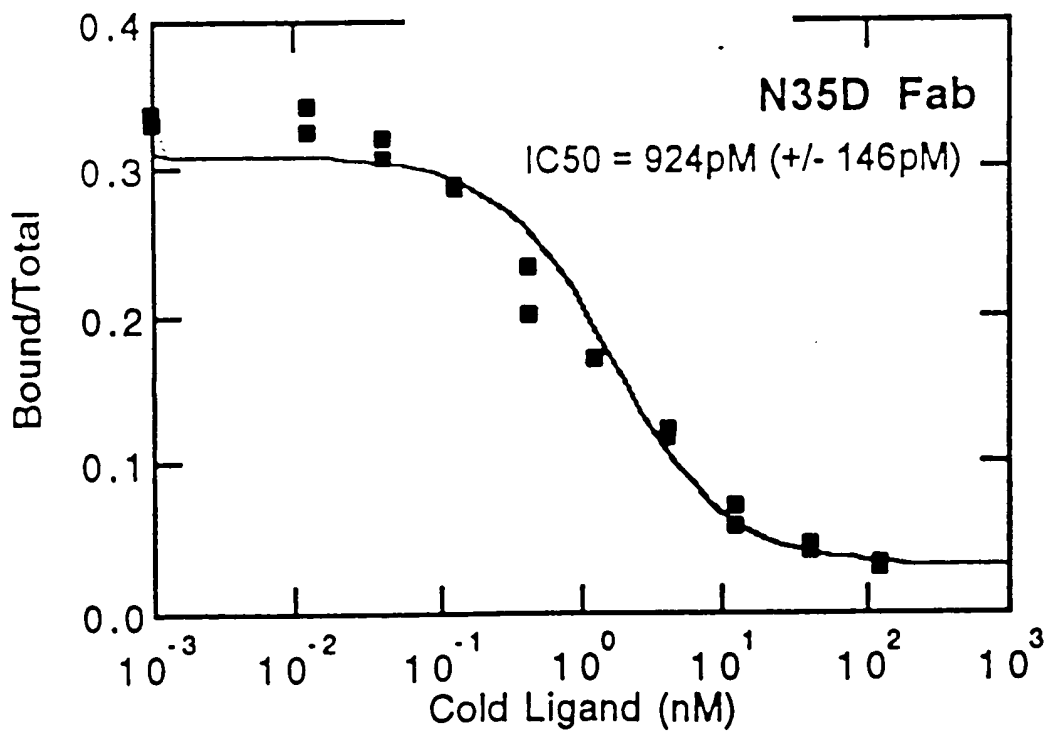


Fig. 43C

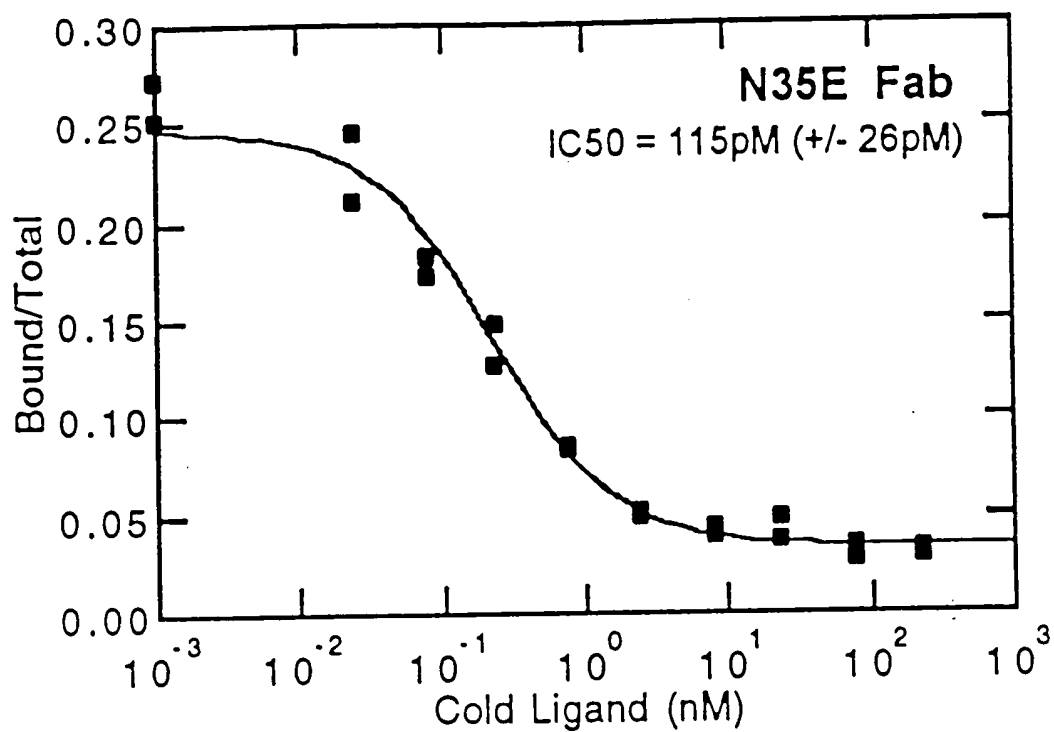


Fig. 43D

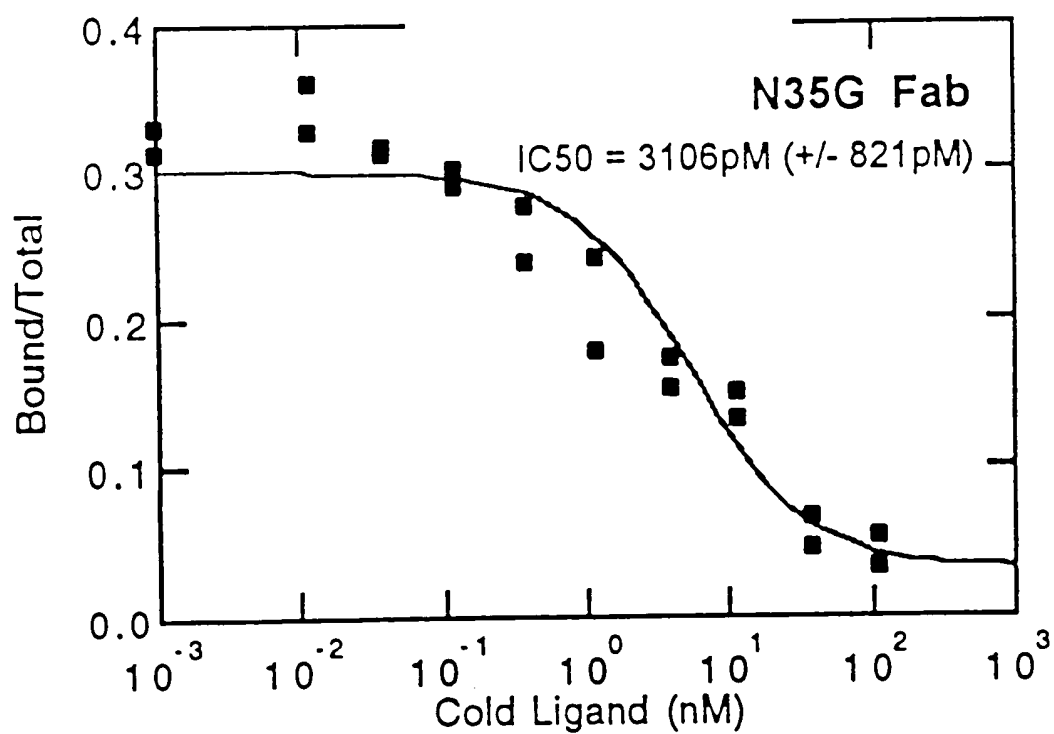
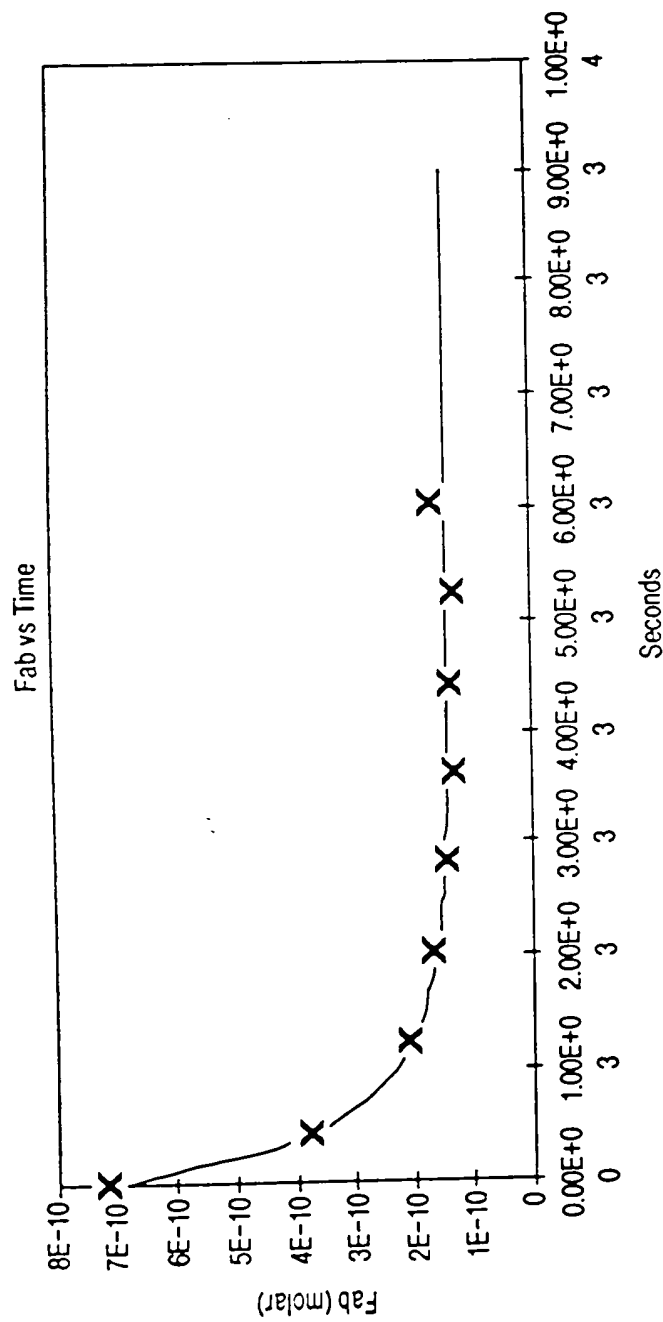


Fig. 43E



Representative Conc versus Time Plot. Shown is the kinetic data for 6G4V11N35A.F(ab')₂.

SAMPLE	ka	kd	Kd
6G4V11N35A-Fab	ND	ND	114pM
6G4V11N35A-F(ab') ₂	2.0x10 ⁶	2.1x10 ⁻⁴	109pM
6G4V11N35E-Fab	4.7x10 ⁶	2.6x10 ⁻⁴	54pM

FIG. 44

1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAC
 TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
 -23 M K K N I A F L L A S M F V F S I A T N

 61 GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCCGCCTC TGTGGGCGAT
 CGTATGCGAC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA
 -3 A Y A D I Q M T Q S P S S L S A S V G D

 121 AGGGTCACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TGAGACGTAT
 TCCAGTGGT AGTGGACGTC CAGTTCAGTT TCGAATCATG TACCATATCC ACTCTGCATA
 18 R V T I T C R S S Q S L V H G I G E T Y

 181 TTACACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC
 AATGTGACCA TAGTTGTCTT TGGTCTTTTT CGAGGCTTTG ATGACTAAAT GTTTCATAGG
 38 L H W Y Q Q K P G K A P K L L I Y K V S

 241 AATCGATTCT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT
 TTAGCTAAGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG CCTAAAGTGA
 58 N R F S G V P S R F S G S G S G T D F T

 301 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC ACAGAGTACT
 GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAAG TGTCTCATGA
 78 L T I S S L Q P E D F A T Y Y C S Q S T

 361 CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA
 GTACAGGGCG AGTGCAAACC TGTCCCATGG TTCCACCTCT AGTTTGCTTG ACACCGACGT
 98 H V P L T F G Q G T K V E I K R T V A A

 421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT
 GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA
 118 P S V F I F P P S D E Q L K S G T A S V

 481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
 CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG
 138 V C L L N N F Y P R E A K V Q W K V D N

 541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
 CGGGAGGTTA GCCCATTGAG GGTCCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCTGTG
 158 A L Q S G N S Q E S V T E Q D S K D S T

 601 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
 ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG
 178 Y S L S S T L T L S K A D Y E K H K V Y

 661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
 CGGACGCTTC AGTGGGTAGT CCCGGACTCG AGCGGGCAGT GTTTCTCGAA GTTGTCCCCT
 198 A C E V T H Q G L S S P V T K S F N R G

 721 GAGTGTTAAG CTGATCCTCT ACGCCGGACG CATCGTGGCC CTAGTACGCA ACTAGTCGTA (SEQ ID NO: 65)
 CTCACAATTC GACTAGGAGA TCGGGCCTGC GTAGCACCAG GATCATGCGT TGATCAGCAT
 218 E C O (SEQ ID NO: 62)

FIG. 45

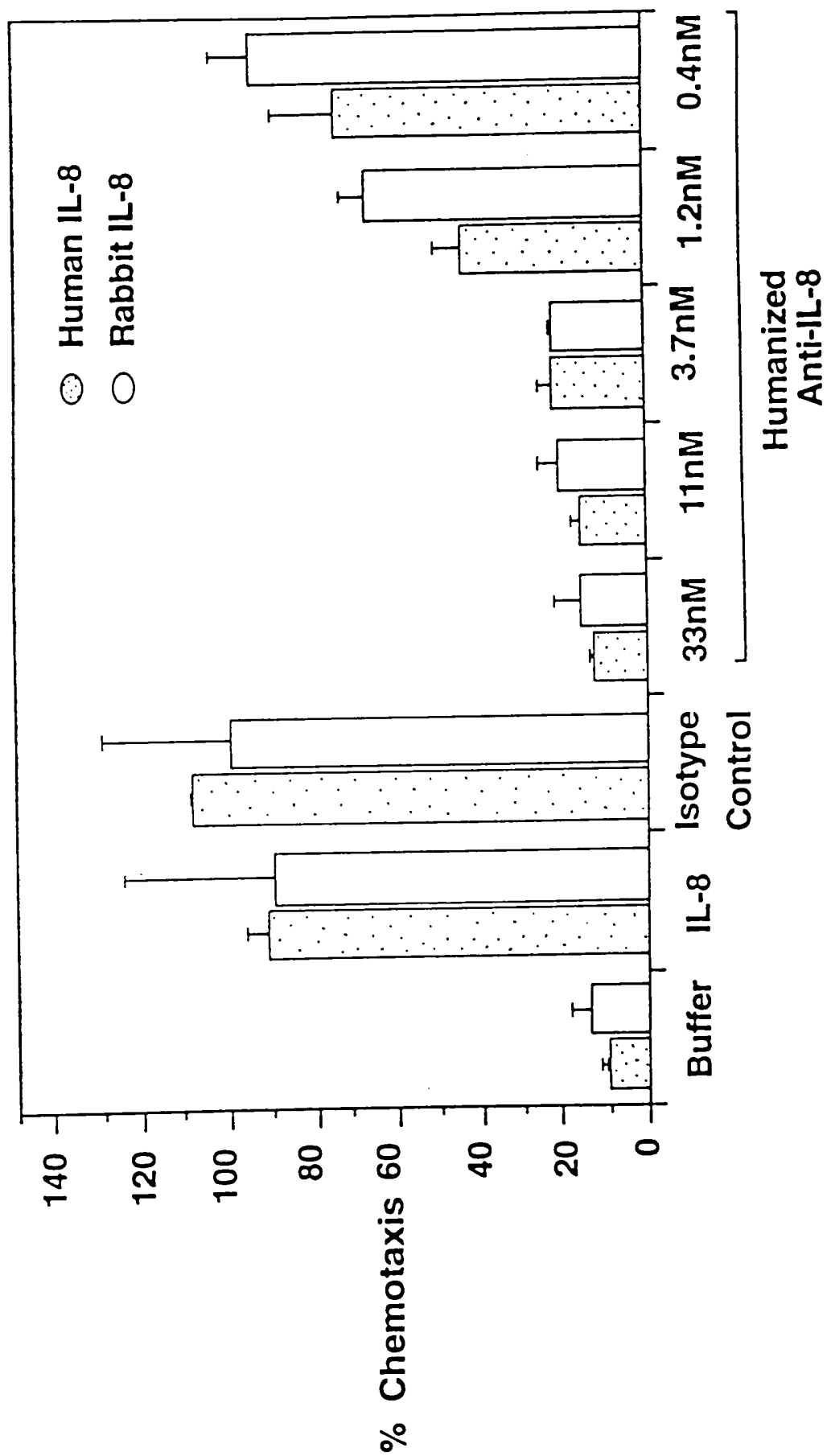


FIG. 46

N35AH1upr

5 CTAGTGCAGTCTGGCGGTGGCCTGGTGCAGCCAGGGGGCTCACTCCGTTTGTCCTGTGCAGCTTCTGGCTACTCCTTC-3' (seq ID NO: 66)

N35AH1lwr

5'-TCGAGAAGGAGTAGCCAGAAAGCTGCACAGGACAAACGGAGTGAGCCCCCTGGCTGCACCAGGCCACCGCCAGACTGCACCT
AG-3'

Bold indicates nucleotide change destroying PvuII site.

FIG. 47

> length: 8120 (circular)
 > This has the pSVI backbone with the pRK7 cloning linker (pSVI7) and the intron DHFR(ID)
 > made from pSVI.WTSD.D by adding a linearization linker(LL) into the HpaI site

```

cac8I
alul
sacI
hgiJII
hgiAI/aspHI
ecII36II
bspI286
bsiHKAI
bmyI
banII
taqI
1 TTCCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGATC GACAGCTGTG GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA
AAGCTCGAGC GGGCTGTAAC TAATAACTGA TCTCAGCTAG CTGTGCACAC CTTACACACA GTCAATCCCA CACCTTTTCAG GGTCCGAGG GGTCGTCGGT

          sau3AI alul
          mboI/ndeII[dam-]
          dpnI[dam+]
          pvuI/bspCI
          pIeI dpnII[dam-]
          hinfI taqI[dam-]
          rmaI mcrI pvuII
          maeI bsiEI nspBII
          bfaI taqI[dam-]
          scrFI
          mvaI
          ecorII
          dsav
          bstNI
          apyI[dcm+]
          bsaJI
          bsmFI nlaIV
          cac8I
          ppulOI
          nsiI/avaIII
          nlaIII
          sphi
          nspi
          nspHI
          cac8I
          sexAI
          bsmFI nlaIV
          cac8I
          CTTCATACGT TTCGTACGTA GAGTTAATCA GTCGTTGGTC CACACCTTC AGGGGTCGGA GGGGTCGTC CAGCAAGTATG CAGCAAGTATG CAGCAAGTATG ATCTCAATTA
          101 GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCCAG GTGTGGAAAG TCCCGAGGCT CCCCAGCAGG CAGCAAGTATG CAGCAAGTATG CAGCAAGTATG ATCTCAATTA
          CTTCATACGT TTCGTACGTA GAGTTAATCA GTCGTTGGTC CACACCTTC AGGGGTCGGA GGGGTCGTC CAGCAAGTATG CAGCAAGTATG CAGCAAGTATG ATCTCAATTA

          acII
          bsmFI
          bsmFI
          acII foki
          acII bsrI acII
          acII bsaJI
          bsaJI dsal
          nlaIII
          styI
          ncoI
          bsII dsal
          acII bsaJI
          CCGCCCCATG GCTGACTAAT TTTTTTTTAT
          CAGTCGTTGG TATCAGGGCG GGGATTGAGG CCGGTAGGCG GGGGTTGAG GCGGTCGAG GCGGGGTAC GCGCTGATTA AAAAAAATAA
  
```

FIG. 48A

[illegible]

FIG. 48B

[illegible]

```

          hgaI
          hinII/acyI
          ahaII/bsaHI
scrFI
mvaI      mnlI
ecorII
dsaV
bstNI     econI
          apyI[dcm+] mnlI
          bsaJI     bslI ddeI
          mnlI
          CTCTCCAGG GTCTCTCTG
          ATACCCAGGC
901 GTGACAAGGA TCATGCAAGG ATTTGAAAGT GACACGTTTT TCCCAGAAAT TGATTTGGGG AATATANAAC CTCTCCAGG ATACCCAGGC GTCTCTCTG
    CACTGTCTCT AGTACGTCTT TAACTTTTCA CTGTGCNAAA AGGCTCTTTA ACTAANCCCC TTTATATTG GAGAGGGTCT TATGGGTCCG CAGGAGAGAC

          nlaIII
          sau3AI
          mboI/ndeII[dam-]
          dpnI[dam+]
          dpnII[dam-]
          maeIII alwI[dam-] apoI      maeIII
          maeIII
          901 GTGACAAGGA TCATGCAAGG ATTTGAAAGT GACACGTTTT TCCCAGAAAT TGATTTGGGG AATATANAAC CTCTCCAGG ATACCCAGGC GTCTCTCTG
    CACTGTCTCT AGTACGTCTT TAACTTTTCA CTGTGCNAAA AGGCTCTTTA ACTAANCCCC TTTATATTG GAGAGGGTCT TATGGGTCCG CAGGAGAGAC

scrFI
mvaI
ecorII
dsaV
bstNI
          apyI[dcm+]
          sau96I
          auaII
          asuI      mnlI      sfaNI      mboII      mnlI      aluI
          1001 AGGTCCAGGA GGAANAAGGC ATCAAGTATA AGTTTGAAGT CTACGAGNAG AAAGACTAAC AGGAACTGTC TTTCAAGTTC TCTGCTCCC TCCTAAAGCT
    TCCAGGTCTC CCTTTTCCG TAGTTCATAT TCAAACTTCA GATGCTCTTC TTCTGTATTG TCCTTCTACG AAAGTTCAG AGACGAGGG AGGATTTCGA
          ^END DHR

          atyI
          bsaJI
          sau3AI
          mboI/ndeII[dam-]
          dpnI[dam+]
          dpnII[dam-]
          alwI[dam-]
          bstYI/xhoII
          cac8I
          dsal bsmFI
          bsaJI
          nlaIII
          styI
          ncoI
          ppulOI
          nslI/avaIII
          1101 ATGCAATTTT ATAAGACCAT GGGACTTTTG CTGGCTTTAG ATCCCTTGG CTTCGTTAGA ACGCAGCTAC AATTAATACA TAACCTTATG TATCATACAC
    TACGTAANA TATTCTGGTA CCCTGANAAC GACCGAATC TAGGGNACC GAAGCAATCT TCGGTCGATG TTAATTATGT ATTGAATAC ATAGTATGTG

          sau96I
          auaII
          asuI
          scrFI
          mvaI
          ecorII

```

FIG. 48D

maeIII hphI scfI foki
 1201 ATACGATTGA GGTGACACTA TAGATAACAT CCACTTTGCC TTTCTCTCCA CAGGTGTCCA CTCCCAAGTC CAACCTGCACC TCGGTTCTAT CGATTCAATT
 TATGCTAAAT CCACTGTGAT ATCTATTGTA GGTGAAACGG NAAGAGAGGT GTCCACAGT balI bsaJI mnlI bsaJI
 dsav bstNI apyI[dcM+] apyI[dcM+] apyI[dcM+] clalI/bspI06
 ecorI taqI apoI
 seq from PRK6G425VH: Cla-AvrII^

nlaIII
 styI
 pflMI
 ncoI
 dsal
 bsaJI foki
 1301 CCACCATGGG ATGGTCATGT ATCATCCTTT TTCTAGTAGC AACTGCMACT GGAGTACATT CAGAAGTTCA GCTAGTGCAG TCTGGCGGTG GCCTGGTGCA
 GGTGGTACCC TACCAGTACA TAGTAGGAAA AAGATCATCG TTGACGTTGA CCTCATGTAA E V Q L V Q S G G G L V Q
 rsaI
 bpaI/gauI[dcM-]
 bsaI csp6I
 rmaI
 maeI
 bfaI
 aluI
 acII haeIII/palI
 bstNI bsoFI
 apyI[dcM+]
 bbaI
 haeI
 scrFI
 mvaI fnu4HI
 ecorII
 dsav

hglJII
 bspI286
 bmyI
 scrFI
 mvaI banII
 ecorII
 dsav
 bstNI
 bsaJI
 apyI[dcM+]

aluI
 alwNI[dcM-]
 fnu4HI
 bsoFI
 bbaI
 hinfI
 taqI
 xhoI
 paeR7I
 avai
 maeIII
 pleI
 sau96I
 avai
 sau96I
 avai
 sau96I
 nlaIV
 sau96I
 haeIII/palI
 sau96I
 sau96I
 nlaIV
 bsaJI
 bstNI
 avai
 bstNI
 scrFI
 nclI
 mspI
 hpaII
 dsav
 cauII
 xmaI/pspAI
 smaI
 scrFI
 nclI
 dsav
 cauII
 bsaJI
 bstNI
 avai
 bstNI
 scrFI
 mvaI
 ecorII
 dsav

1401 GCCAGGGGGC TCACCTCGTT TGTCCTGTGC AGCTTCTGGC TACTCTCTCT CGAGTCACTA TATGCACTGG GTCCGTCAGG CCCCAGGTAA GGCCTGGAA
 CCGTCCCCCG AGTGAGGCAA ACAGGACCG TCGAGACCG ATGAGGACCG GTCACTGAT ATACGTGACC CAGGCAGTCC GGGGCCCATT CCGGACCTT
 14 P G G S L R L S C A A S G Y S F S S H Y M H W V R Q A P G K G L E

FIG. 48E

bslI
 sau3AI
 mboI/ndeII[dam-]
 dpnI[dam+]
 dpnII[dam-]
 alwI[dam-] hphI
 1501 TGGGTTGGAT ATATTGATCC TTCCAAATGGT GAAACTACGT ATATCAAAA GTTCAAGGCG CGTTTCACTT TATCTCGCGA CAACTCCAAA AACACAGCAT
 ACCCAACCTA TATAACTAGG AAGGTTACCA CTTTGATGCA TATTAGTTT CMAAGTTCCG GCNAAGTGAA ATAGAGCGCT GTTGAGGTTT TTGTGTCGTA
 47 W V G Y I D P S N G E T T Y N Q K F K G R F T L S R D N S K N T A Y
 hnlI/acyI
 ahall/bsaHI
 aatII
 bsRI
 maeIII
 taqI
 hphI
 mboII
 maeII
 1601 ACCTGCAGAT GAACAGCCTG CGTGCTGAGG ACACCTGCGT CTATTACTGT GCNAGAGGGG ATTATCGCTA CAATGGTGAC TGGTTCTTCG ACGTCTGGGG
 TGGAGCTCTA CTTGTCGAC GCACGACTCC TGTGACGCA GATAATGACA CGTTCTCCCC TAATAGCGAT GTTACCACATG ACCAAGAAGC TGCACACCCC
 81 L Q M N S L R A E D T A V Y Y C A R G D Y R Y N G D W F F D V W G
 scrFI
 mvaI
 ecorII
 dsav
 batNI
 sau96I
 nlaIV
 hglI
 bsp120I
 bmyI
 banII
 asuI
 mboII
 bpuAI
 apaI
 styI
 bsaJI
 mnlI
 haeII/pali
 haeII/aspHI
 bseRI
 bsp1286
 apyI[dcm+] mnlI
 bmyI mnlI
 bsaJI
 TCCACAGACA CCTCTGGGG CACAGCGGCC
 1701 TCNAGGAACC CTGGTCACCG TCTCCTCGGC CTCCACCMAG GGCCCATCGG TCTTCCCCCT GGCACCTCC TCCACAGACA CCGTGGGAGG AGGTTCTCGT GGAGACCCCC GTGTCGCCGG
 AGTTCTTGG GACCACTGGC AGAGGAGCCG GAGGTGGTTC CCGGGTAGCC AGACGGGGA CCGTGGGAGG AGGTTCTCGT GGAGACCCCC GTGTCGCCGG
 114 Q G T L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A
 hnu4HI
 bsoFI
 bsp1286 aciI bsaJI
 bmyI nspBII apyI[dcm+]

FIG. 48F

[illegible]

FIG. 48G

sau96I
nlaIV
mspI
hpaII
scrFI
ncII
dsaV

sau3AI avaiI nlaIII
mboI/ndeII[dam-] nspl
nlaIII cauII mnlI nspHI
rcal dpmI[dam+] ddei mali
mnlI dpmII[dam-] eco8II maeII
mali bspHI[dam-] asuI bsu36I/mstII/sauI
GGACACCCTC ATGATCTCCC GGACCCCTGA GGTCAACATGC GTGCTGGTGG maeII
CGAAGACCCCT GAGTCAAAGT
247 L F P P K P K D T L M I S R T P E V T C V V V D V S H E D P E V K F

mboII styI
earI/kap632I bsaJI
CTCTTCCCCC CAATAACCCAA GGACACCCTC ATGATCTCCC GGACCCCTGA GGTCAACATGC GTGCTGGTGG maeII
GAGAAGGGGG GTTTGGGTT CCTGTGGGAG TACTACAGGG CCTGGGACT CCAGTGATCG CACCACCACC TGCACCTCGT GCTTCTGGGA CTCCAGTTCA

acII
thaI
fnuDII/mvni
bstOI
bsl1236I
sacII/asII
napBII
kspI
dsal
bsaJI
maeII
rsal
cap6I
barI bsaAI
fnu4HI mnlI
fnu4HI mnlI
bsOFI bsaRI
bsOFI cap6I
rsal
cap6I
maeII
bsaAI
rsal
cap6I
hphI
hgaI mnlI

2201 TCAACTGGTA CGTGGACGGC GTGGAGGTGC ATAATGCCAA GACAAGCCCG CGGGAGGAGC AGTACAACAG CACGTACCGT GTGGTCAGCG TCCTCACCGT
AGTTGACCAT GCACCTGCCG CACCTCCACG TATTACGGTT CTGTTTCGGC GCCCTCCTCG TCATGTTGTC GTGCATGGCA CACCAGTCGC AGGAGTGCCA

281 N W Y V D G V E V H N A K T K P R E E Q Y N S' T Y R V V S V L T V

scrFI
mvaI
ecoRII
dsaV

econI bstNI barI
balI apyI[dcam+]
CCTGCACCAG GACTGGCTGA ATGGCAAGGA GTACMAGTGC MAGGTCTCCA ACNAGCCCT CCCAGCCCCC taqI
GGACGTGGTC CTGACCGACT TACCGTTCTC CATGTTTCAG TTCCAGAGGT TGTTTCGGGA GGTTCGGGG TAGCTCTTTT I S K A K G

2301 CCTGCACCAG GACTGGCTGA ATGGCAAGGA GTACMAGTGC MAGGTCTCCA ACNAGCCCT CCCAGCCCCC taqI
GGACGTGGTC CTGACCGACT TACCGTTCTC CATGTTTCAG TTCCAGAGGT TGTTTCGGGA GGTTCGGGG TAGCTCTTTT I S K A K G

314 L H Q D W L N G K E Y K C K V S N K A L P A P I E K T I S K A K G

fnu4HI
bsaFI
bbvI
agccaaaggg
tcggtttccc

scrFI
ncII
mapI
hpaII
dsaV
cauII
xmaI/pspAI
smaI
scrFI
ncII
dsaV
cauII
fokI
bsaI bsaJI mboII
csp6I
bapI407I/bsrGI bslI auaI earI/ksp632I
avaI
2401 CAGCCCCGAG AACACACAGGT GTACACCCCTG CCCCCATCCC GGGAGAGAGAT GACCAAGAAC CAGGTCAGGC TGACCTGCCT GGTCAAAGGC TTCTATCCCA
GTCCGGGCTC TTGGTGCCA CATGTGGGAC GGGGGTAGGG CCCTTCTCTA CTGGTTCTTG GTCCAGTCGG ACTGCAGTCGG CCAGTTTCCG AAGATACGGT
347 Q P R E P Q V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P S
mspI
hpaII
fnu4HI
bsaFI
bavI
bsaJI
malI bsaJI
2501 GCAGATCGC CGTGGAGTGG GAGAGCAATG GGCAGCCCGA GAACAACTAC AAGACACAGC CTCCCGTGCT GGACTCCGAC GGCTCTTCT TCCTCTACAG
CGCTGTAGGC GCACCTCACC CTCTCGTAC CGCTCGGCT CTGTGTGATG TTCTGTGTCG GAGGGACGA CTTGAGGCTG CCGAGGAAGA AGGAGATCTC
381 D I A V E W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S
mboII
bpuAI
fnu4HI
bsaFI
bavI
bsaJI
malI bsaJI
414 K L T V D K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L

sau96I
 acII haeIII/palI
 fnu4HI asuI
 bsoFI nlaIII
 sfilI styI
 eaeI ncoI
 cfrI dsal
 aluI haeIII/palI
 hindIII bglI bsaJI
 aluI haeIII/palI
 hindIII bglI bsaJI
 asuI bfaI accI bspMI
 haeIII/palI bsgI
 sau96I hinfI pstI
 maeI hincII/hindII
 rmaI salI scfI
 pleI
 taqI
 bsmAI
 balI cauII
 bali cauII
 TCCCTGTCTC CGGGTAAATG AGTGGACGG CCCTAGAGTC GACCTGCAGA AGCTTGGCGG CCATGGCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTTACA
 AGGGACAGAG GCCCATTTAC TCAGGCTGCC GGGATCTCAG CTGGACGTCT TCGMACCGGC GGTACCGGGT TGNACAAATA ACGTCGAATA TTACCAATGT
 447 S L S P G K O (524 bp NO: 71)
 afanI apoI
 nlaIII aluI(dam-)
 2801 AATAAAGCMA TAGCATCACA AATTTCACMA ATAAAGCATT TTTTCACTG CATCTAGTT GTGGTTTGT CAAACTCATC AATGTATCTT ATCATGTCTG
 TTATTTCGTT ATCGTAGTGT TTTAAGTGT TATTTCTGTA AANAAGTGAC GTAAGATCAA CACCAACACG GTTGGAGTAG TTACATAGAA TAGTACAGAC
 sau3AI
 mboI/ndeII(dam-)
 dpnI(dam+)
 dpnII(dam-)
 pvuI/bspCI
 mcrI
 baeII
 taqI(dam-) tru9I
 clai/bsp106(dam-)
 bspDI(dam-) mseI
 sau3AI xmnI
 mboI/ndeII(dam-)
 dpnI(dam+) asp700
 dpnII(dam-) aseI/asnI/vspI
 baeII
 fnu4HI haeI
 bsoFI styI
 bbvI ncoI
 hinPI dsal haeIII/palI
 hhaI/cfoI nlaIII
 bsaJI
 rsaI
 csp6I
 nlaIV
 kpnI
 hgiCI
 bsaI
 asp718 mnlI
 acc65I ddeI acII
 2901 GATCGATCGG GAATTAAATC GCGCAGCAC CATTGGCTGTA AATAACCTCT GMAAGAGGNA CTTGGTTAGG TACCTTCTGA GGCGGAAGA ACCATCTGTG
 CTAGCTAGCC CTTAATTAG CCGGCTCGT GTACCGGACT TTATTGGAGA CTTTCTCCTT GAACCAATCC ATGGAAGACT CCGCCTTCT TGGTAGACAC

3001 GAATGTGTGT CAGTTAGGCT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA GRAGTATGCA AACGATGCAT CTCATTAGT CAGCAACCAG GTGTGGAAAG CTTACACACA GTCAATCCCA CACCTTTCAG GGGTCCGAGG GGTCGTCCGT CTTCATACGT TTCTGACGTA GAGTTAATCA GTCGTTGGTC CACACCTTTC

3101 TCCCGAGGCT CCCAGCAGG CAGAAGTATG CANAGCATGC ATCTCAATTA GTCAGCAACC ATACTCCCG CCCTAACTCC GCCATCCG CCCCTAACTC AGGGGTCCGA GGGGTCCGTC GTCTTCATAC GTTTCGTAGC TAGAGTTAAT CAGTCGTTGG TATCAGGCG GGGATTGAGG CGGGTAGGCG GGGGATTGAG

3201 CGCCAGTTC CGCCCATTTCT CGGCCCATG CGGCCCATG GCGGGTCAAG GCGGGTAAGA GCGGGGTAC CGACTCATTA AAAAAATAA ATACGTCTCC GGCTCCGCG GAGCCGGAGA CTCGATAAGG TCTTCATCAC

[illegible][illegible][illegible]

FIG. 48M

mspl
 hpall
 bsli
 bsaWI
 sau3AI
 mboI/ndeII[dam-]
 dpmI[dam+]
 dpmII[dam-]
 alwI[dam-]
 nlaIV
 batYI/xhoII
 bamHI
 alwI[dam-]
 bsmFI
 TCTCTGGATC CGTTCTGGG ACGGATTTC CTCTGACCAT CAGCAGTCTG
 AGACACCTAG GCCAAGACCC TGCCTAAGT GAGACTGGTA GTCGTCAGAC
 G S G S G T D F T L T I S S L
 rsal
 csp6I
 nlaIV
 kpnI styI
 hgiCI
 bani bsaJI
 asp7I8
 acc65I
 GGACAGGGTA CCAAGGTGGA
 CCTGTCCCAT GGTCCACCT CTAGTTGCT TGACACCGAC
 G Q G T K V E I K R T V A A
 mboII
 bpuaI
 bbsI
 CAGCCAGAAG ACTTCGCAAC TTATTACTGT TCACAGAGTA CTCATGTCCC GCTCAGGTTT maeII
 GTGGGTCTTC TGAAGCGTTG AATAATGACA AGTGTCTCAT GAGTACAGG CGAGTGCAA L T F
 H V P L T F
 mboII
 bpuaI
 bbsI
 CACCATCTGT CTTTCATCTTC CGCCCATCTG ATGAGCAGTT GAATCTGGA ACTGCTTCTG
 GTGGTAGACA GAAGTAGAAG GCGGTAGAC TACTCGTCAA CTTTAGACCT TGACGAGAC AACACACGGA CGACTTATTG AAGATAGGT CTCTCCGTT
 P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E A K
 xmnI
 asp700
 cac8I
 xmnI
 asp700
 haeII
 mnlI
 haeIII/palI

FIG. 48N

4101 AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAACTGCCAGGAGA GTGTCAACAGA GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC
 151 V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S T
 4201 CTGAGCTGA GCAAGCAGA CTACAGAAA CACAAGTCT ACGCCTGCGA AGTCACCCAT CAGGGCCTGA GCTGCCCGT CACAAGAGC TTCAACAGGG
 184 L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R G
 4301 GAGAGTGTTA AGCTGGCCG CCATGGCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTACA AATAAGCAA TAGCATCACA AATTTCACA AATAAGCATT
 218 E C O (seq ID no: 72)

FIG 48D

4701 ATCTCAATTA GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG CCCCTAACTC CGCCAGTTC CGCCATTCT CGCCCATG GCTGACTAAT
TAGAGTTAAT CAGTCGTTGG TATCAGGGCG GGGATTGAG CGGGTAGGGC GGGGATTGAG GCGGGTCAAG GCGGGGTAC GCGACTGATTA

4801 TTTTITTTTATT TATGCAGAGG CCGAGGCGCG CTCGGCTCT GAGCTATTCC AGAGTACTG AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAAGCTG
AAAAAATAA ATAGTCTCC GGCTCCGGCG GAGCGGAGA CTCGATAAGG TCTTCATCAC TCCTCCGAA AACCTCCG ATCCGAAAC GTTTTCGAC
start pUC118~

4901 TTACCTCGAG CGCGCGCTTA ATTAGCGCG GCCATTNAA TCCTGCAGGT AACAGCTTGG CACTGGCCGT CGTTTACAA CGTCGTGACT GGGAAACCC
AATGGAGCTC GCGCGGAAT TAATTCGCG CGGTAAATTT AGGAGCTCCA TTGTGAAACC GTGACCGCA GCAATATGTT GCAGCACTGA CCCTTTTGGG

^linearization linker inserted into HpaI site

[illegible]

FIG. 48B

mspI
hpaII
naeI
cfr101/bsrFI
maeII cac8I
5301 TTTCTCGCCA CGTTCGCCG CTTTCCCGT CAAAGCTTAA ATCGGGGGCT CCCTTTAGG TTCCGATTGA GTGCTTTACG GCACCTCGAC CCCAAAAAAC
AAGAGCGGT GCAAGCGGCC GAAAGGGCA GTTCGAGATT TAGCCCCCGA GGGAAATCCC AAGGCTAAT CACGAAATGC CGTGGAGCTG GGGTTTTTTC
nlaIV
hgiCI taqI
bani mnlI
nlaIV
maeII haeIII/palI
draIII sau96I
5401 TTGATTTGGG TGATGGTTCA CGTAGTGGC CATCGCCCTG ATAGACGGTT TTTGGCCCTT TGACGCTTGA GTCCACGTTT TTTAATAGTG GACTCTTGT
AACTAAMCCC ACTACCAAGT GCATCACCG GTAGCGGAC TATCTGCCA AAGCGGGA ACTGCNACCT CAGGTGCAAG AAATATATAC CTGAGAACNA
hphI
bsaAI asuI
bsrI
bslI
5501 CCAAACTGGA ACACACTCA ACCCTATCTC GGGCTATTCT TTTGATTTAT AAGGATTTT GCCGATTTCG GCCTATTGGT TAAAAAATGA GCTGATTTAA
GGTTTGACCT TGTGTGAGT TGGGATAGAG CCGGATAAGA AACTAATA TTCCCTAATA CCGCTAAGC CGGATAACCA ATTTTACT CGACTAAAT
truDII/mvni
trugI apoI tru9I
mseI bstUI mseI
apoI bsh1236I sspI mseI
5601 CAAAAATTGA ACGCAATTT TAACAAATA TTAACGTTTA CAATTTTATG GTGCACTCTC AGTACAATCT GCTCTGATGC CGCATAGTTA AGCCAATCC
GTTTTAAAT TGCCTTAA ATTGTTTTAT AATTGCAAT GTTAAATAT CACGTGAGAG TCATGTTAGA CGAGACTAGC GCGTATCAAT TCGGTTGAG
thai
fnuDII/mvni
trugI apoI tru9I
mseI bstUI mseI
apoI bsh1236I sspI mseI
5601 CAAAAATTGA ACGCAATTT TAACAAATA TTAACGTTTA CAATTTTATG GTGCACTCTC AGTACAATCT GCTCTGATGC CGCATAGTTA AGCCAATCC
GTTTTAAAT TGCCTTAA ATTGTTTTAT AATTGCAAT GTTAAATAT CACGTGAGAG TCATGTTAGA CGAGACTAGC GCGTATCAAT TCGGTTGAG
maeIII
maeII bari
bsaAI tth1111/aspI bbvI
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCCCGGACG CCGCCAGAC CCCTGACGC GCCCTGACGG GCTTGCTGTC TCCCGCATC CGCTTACAGA
CGATACGGAT GCACTGACCC ACTACCGAG CCGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGAC GCGGCGGTAG GCGAATGTCT
hinPI
fnu4HI
bsaFI
nlaIII hhaI/cfoI
bsaFI
tth1111/aspI bbvI
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCCCGGACG CCGCCAGAC CCCTGACGC GCCCTGACGG GCTTGCTGTC TCCCGCATC CGCTTACAGA
CGATACGGAT GCACTGACCC ACTACCGAG CCGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGAC GCGGCGGTAG GCGAATGTCT
hinPI
fnu4HI
bsaFI
nlaIII hhaI/cfoI
bsaFI
tth1111/aspI bbvI
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCCCGGACG CCGCCAGAC CCCTGACGC GCCCTGACGG GCTTGCTGTC TCCCGCATC CGCTTACAGA
CGATACGGAT GCACTGACCC ACTACCGAG CCGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGAC GCGGCGGTAG GCGAATGTCT

FIG. 48S

FIG 48T

6301 GCTATGTGGC GCGGTATTAT CCCGTTGATGA CGCCGGGCNA GAGCAACTCG GTCCGCCGCAT ACACCTATTCT CAGAATGACT TGCTTGAGTA CTCACCAGTC
CGATACACCG CGCCATAATA GGGCACTACT CGGCCCGCT CTGCTTGAGC CAGCGCGGTA TGTGATNAGA GTCTTACTGA ACCAATCAT GAGTGGTCAG

6401 ACAGAAAGC ATCTTACGGA TGGCATGACA GTAAGAGAAAT TATGCAGTGC TGCCATAACC ATGAGTGATA ACACCTGGCG CAACCTACTT CTGACAACGA
TGCTCTTTCG TAGAATGCCT ACCGTACTGT CATCTCTCTTA ATACGTACCG ACGGTATGG TACTCACTAT TGTGACGCCG GTTGAATGAA GACTCTTGCT

6501 TCGGAGACC GAAGAGCTA ACCGCTTTTT TGCAACACAT GGGGATCAT GTAACTCGCC TTGATCGTTG GGAAACGGAG CTGNATGAG CCATACCAAA
AGCCTCCTGG CTCTCTCGAT TGGCAAAA ACGTGTTGTA CCCCCTAGTA CATTGACCG CATTGACMAC CCTTGGCCTC GACTTACTTC GGTATGTTT

[illegible]

FIG. 48V

sau3AI
mboII[dam-]
sau3AI mboI/ndeII[dam-] theI fnuDII/mvni
mboI/ndeII[dam-] bstUI cac8I
dpmI[dam+] dpmI[dam+] fnu4HI
dpmII[dam-] dpmII[dam-] bshI236I fsoFI
bstYI/xhoII alwI[dam-] hlnPI
bstYI/cfoI hhaI/cfoI bbvI
alwI[dam-] bstYI/xhoII
7101 TCAAGGATC TTCTTGAGAT CCTTTTTTC TGCGCGTAAT GACGACGAAC GTTTGTTTTT CAAACMAAA AACACCGGT ACCAGCGGT GTTGTGTTGC CGGATCAAGA
AGTTTCCTAG AAGNACTCTA GGAATAAAG ACGCGCATTA GCGCGCTGCT GAGTATGACA GGAATACTGT CCTTCTAGTG TAGCGTAGT TAGCGACCA CTTCAGAAC
7201 GCTACCAACT CTTTTCCGA AGTAACTGG CTTACAGACA GCGCAGATAC CMAATACTGT CCTTCTAGTG TAGCGTAGT TAGCGACCA CTTCAGAAC
CGATGGTTGA GAAAAGGCT TCCATTGACC GAGTCTGCT CCGCTCTATG GTTTATGACA GGAATACTGT CCTTCTAGTG TAGCGTAGT ATCCGCTGGT GAAGTCTTG
7301 TCCTAGCAC CGCTACATA CTCGCTCTG CTAATCCTGT TACCAGTGGC TGCTGCCAGT GCGGATAGT CGTGTCTTAC CGGTTGAC TCAGACCAT
AGACATCGTG CGCGATGAT GGACGAGAC GATTAGGACA ATGGTCAACC ACGACGGTCA CCGCTATTCA GCACAGATG GCCCAACCTG AGTTCTGCTA
7401 AGTTACCGA TAAGGCGCAG CGCTCGGGCT GAACGGGGG TTCGTGCACA CAGCCAGCT TGGAGCGAAC GACCTACACC GAACGTAGAT ACCTACAGG
TCATGGGCT ATTCCGCTC GCAGCCCCG CTTGCCCCCG AAGACGCTGT GTCGGGTGCA ACCTCGCTTG CTGGATGCG CTTGACTCTA TGGATGCTG

7501 TGAGCATTTGA GAAAGCGCCA CGCTTCCCGA AGGAGAGAAAG GCGGACAGGT ATCCGGTAAAG CGGCACGGTC GGAACAGGAG AGCGACGAG GGAGCTTCCA
 ACTCGTNACT CTTTCGGCGT CGNAGGGGCT TCCCTCTTTC 'GGCTGTCCA TAGGCCATTC GCGGTCCAG CCTTGCTCTC TCGCGTGCTC CCTCGAAGGT
 scrFI mvaI ecorII dsav
 hinPI hhaI/cfoI
 haeII
 mspI fnu4HI
 hpaII bsaI bsoFI
 bsaWI aciI
 bbsSI hinPI mnlI
 hhaI/cfoI aluI apyI(dcm+)

7601 GGGGGAAACG CCTGGTATCT TTATAGTCCT GTCGGGTTTC GCCACCTCTG ACTTGAGCGT CGATTTTGTGATGCTCGTC AGGGGGCGCG AGCCTATGGA
 CCCCCCTTGC GGACCATAGA AATATCAGGA CAGCCCAAG CCGTGGAGAC TGAACCTCGCA GCTAAAAACA CTACGAGCAG TCCCCCGGCC TCGGATACCT
 scrFI mvaI ecorII dsav bstNI
 haeIII/pali
 apyI(dcm+) mnlI drdI hgaI
 nlaIV
 aciI
 sfaNI

7701 AAAAGCCGAG CAACCGGCC TTTTACGGT TCCTGGCCTT TTGCTGGCCT TTTGCTCACA TGTTCTTCC TCGGTTATCC CCTGATTCTG TGGATAACCG
 TTTTGGCGTC GTTGGCGCGG AAAAATGCCA AGGACCGGAA AACGACCGGA AACGAGTGT ACAGAAAGG ACCGAATAGG GGACTAAGAC ACCTATTGGC
 scrFI fnu4HI bsoFI
 cac8I bsh1236I nlaIV haeI cac8I
 haeIII/pali
 fnu4HI scrFI mvaI bsaI
 ecorII
 dsaV
 haeI
 haeIII/pali nspI
 nlaIII
 thaI bsaI
 fnuDII/mvnl
 bstUI
 apyI(dcm+) haeI
 afliII
 tfII
 hinFI

7801 TATTACCGCC TTTGAGTGAG CTGATACCGC TCGCGCGCAGC CGAACGACCG AGCGAGCGGA GTCACTGAGC GAGGAGCGG AAGAGCGGCC AATACGCMAA
 ATATATGGCGG AACTACTC GACTATGGCG AGCGCGTGC GCTTGCTGGC TCGCGTGGCT CAGTCACTGC CTCCTTGGCC TTCTCGCGGG TTATCGGTTT
 scrFI fnu4HI bsoFI
 cac8I aciI
 bsrBI fnu4HI mcrI hlnPI hlnfi
 bsoFI
 hhaI/cfoI
 haeII
 mnlI aciI
 sapi hlnPI
 mboII hhaI/cfoI
 earI/ksp632I

FIG. 48X

```

    thal
    fnuDII/mvnI
    bstUI
    bsh1236I
    hinPI
    hhal/cfoI
    thal
    fnuDII/mvnI          cac8I
    bstUI haeIII/palI    aluI
    bsh1236I          tru9I pvuII
    bslI  caeI  tfII ael/asnI/vspI
    acII  cfrI  hinfI mscI  napBI
    7901 CCGCCTCTCC CCGCGGCTTG GCCGATTTCAT TAATCCAGCT GGCACGACAG GTTCCCGAC TGGAAAGCGG GCAGTGAGCG CAACGCAATT AATGTGAGTT
    GCGGAGAGG GCGCGGCAC CCGCTAAGTA ATTAGGTCA ATTAGGTCA CCGTGCTGTC CAAAGGGCTG ACCTTTCCGC CGTCACTCGC GTTGGGTTAA TTACACTCAA

    scrFI
    mvaI
    ecoRII
    dsav
    nlaIV bstNI
    hgiCI apyI(dcm+)
    banI bsaJI
    8001 ACCTCACTCA TTAGGCACCC CAGGCTTTAC ACTTTATGCT TCCGGCTCGT ATGTTGTGTG GAATTGTGAG CGGNTAACAA TTTCACACAG GAAACAGCTA
    TGGAGTGAGT AATCCGTGGG GTCCGAATG TGAATACGA AGGCCGAGCA TACAACACAC CTTAACACTC GCCTATTGTT AAAGTGTC CTTGTGCGAT
    aluI

```

FIG. 48Y

```

tru9I
mseI
aseI/asnI/vspI
xmnl
nlaIII asp700
8101 TGACCATGAT TACGAATTAA (SEQ ID NO:68)
ACTGGTACTA ATGCTTAATT

>length: 8120

aatII(GACGTC): 1690 5947
acc65I(GGTACC): 2969 3967 4529
accI(GTAKAC): 823 1039 2738 4237
acII(CCGC): 217 229 238 250 260 271 317 422 454 485 574 1385 1795 1871 2248 2250 2758 2982
3167 3179 3188 3200 3210 3221 3267 3372 3404 3449 3686 3949 4021 4318 4542 4727
4739 4748 4760 4770 4781 4827 4910 4914 5070 5127 5153 5166 5203 5217 5220 5248
5275 5680 5699 5741 5751 5790 5979 6026 6125 6234 6311 6355 6476 6522 6713 6804
7166 7175 7310 7420 7541 7560 7687 7715 7806 7827 7834 7877 7901 7911 7967 8070

acyI
see hinII
afIII/bfII(CTTAAG): 786
afIII(ACRYGT): 932 7758
ageI(ACCGGT): 1833
ahaII/baaHI(GRCGYC): 988 1690 1858 5117 5947 6329
ahaII/draI(TTTAAA): 696 4935 6290 6982 7001
ahdI/eamII05I(GACNNNNNGTC): 2087 6865
aluI(AGCT): 5 44 332 386 390 753 1097 1165 1370 1431 1951 2603 2751 2784 3282 3336 3340
3562 3566 3676 3733 3792 4270 4288 4311 4344 4554 4842 4896 4954 5047 5333 5590
5803 5822 6516 6579 6679 7200 7457 7593 7819 7937 8096
alw44I/anoI(GTGCAC): 1876 5651 6198 7444

```

FIG. 48Z

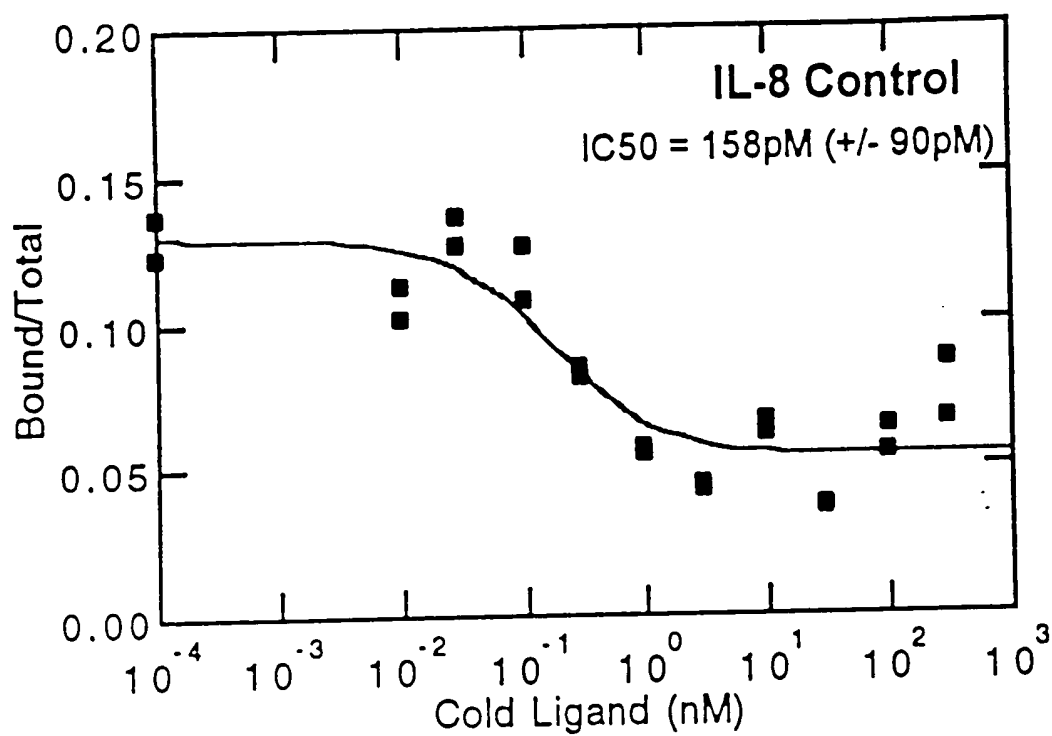


FIG. 49A

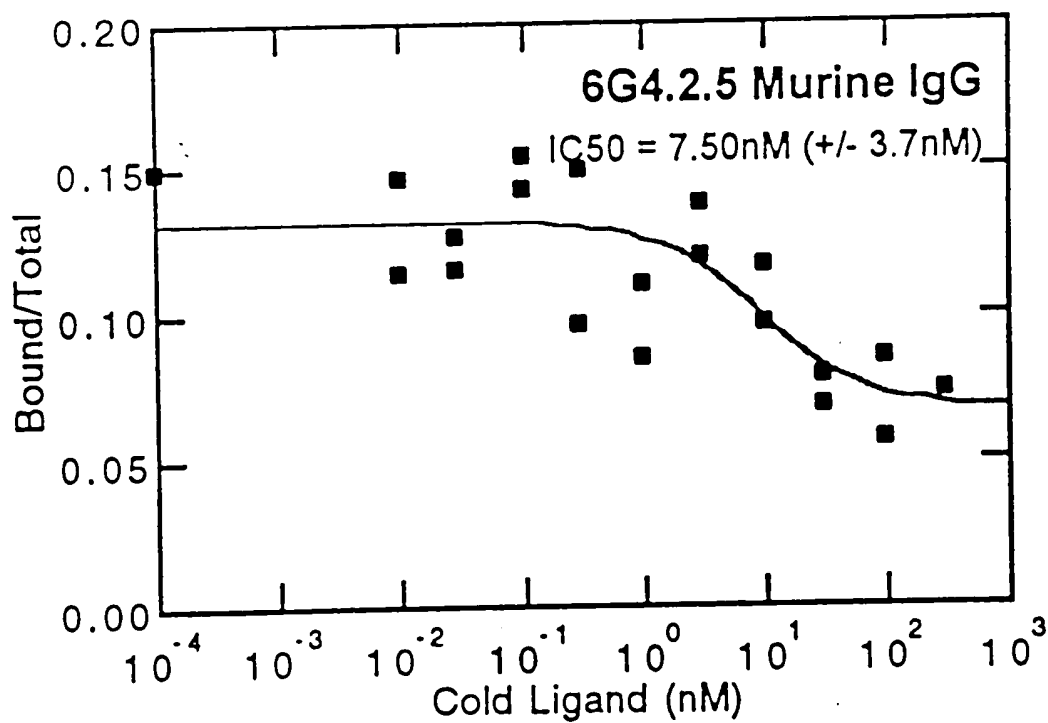


FIG. 49B

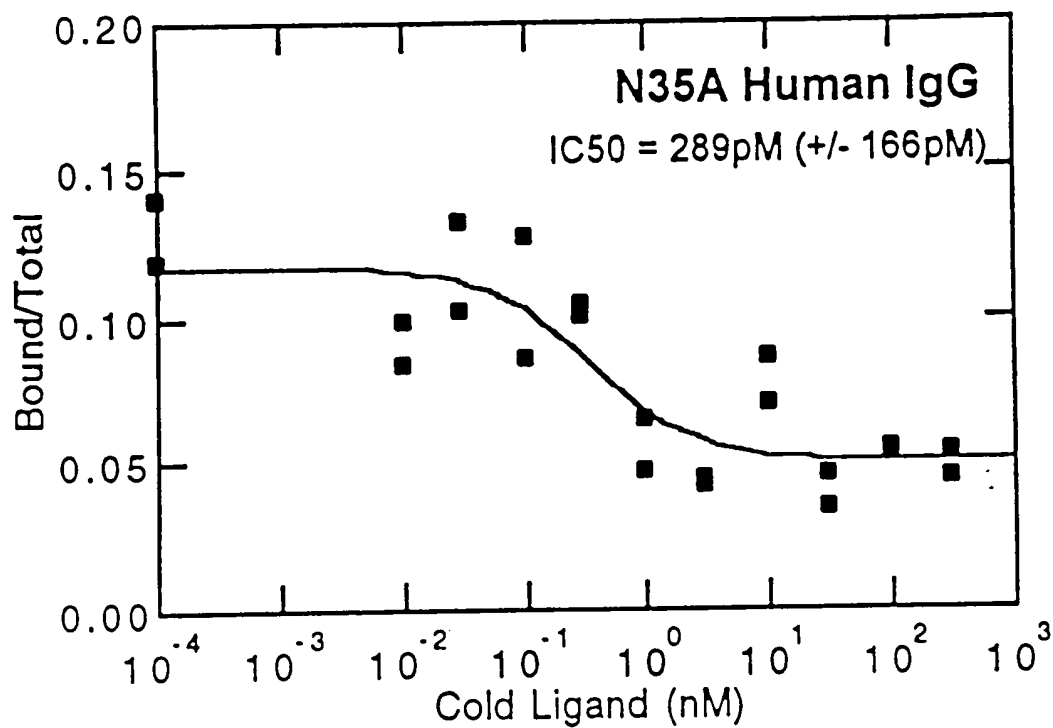


FIG. 49C

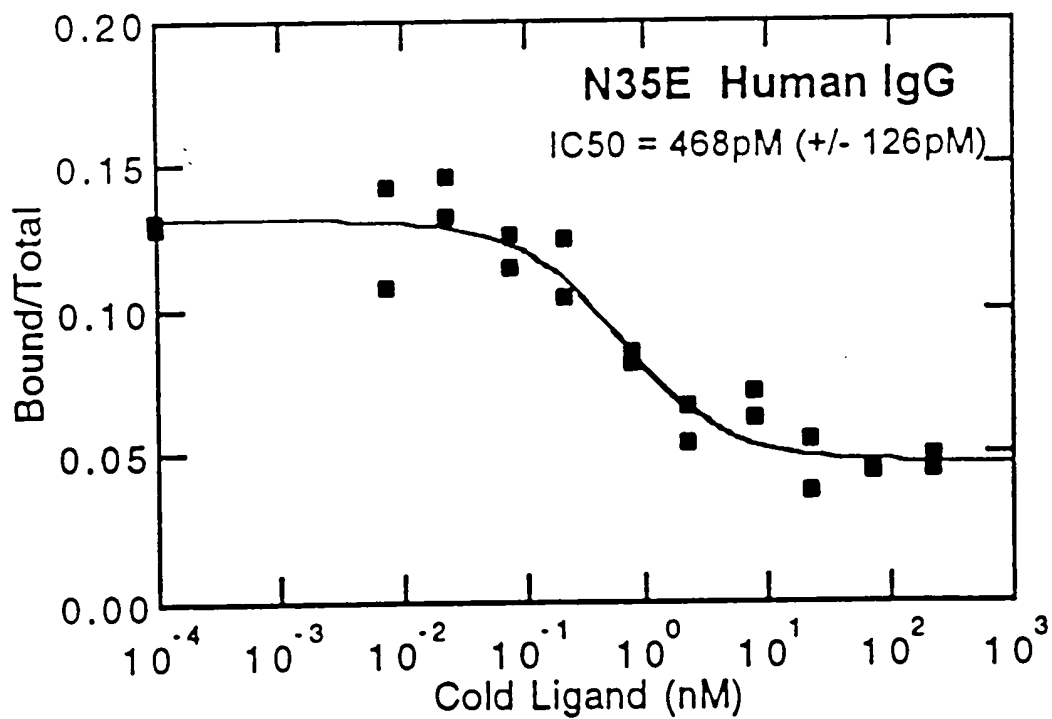


FIG. 49D

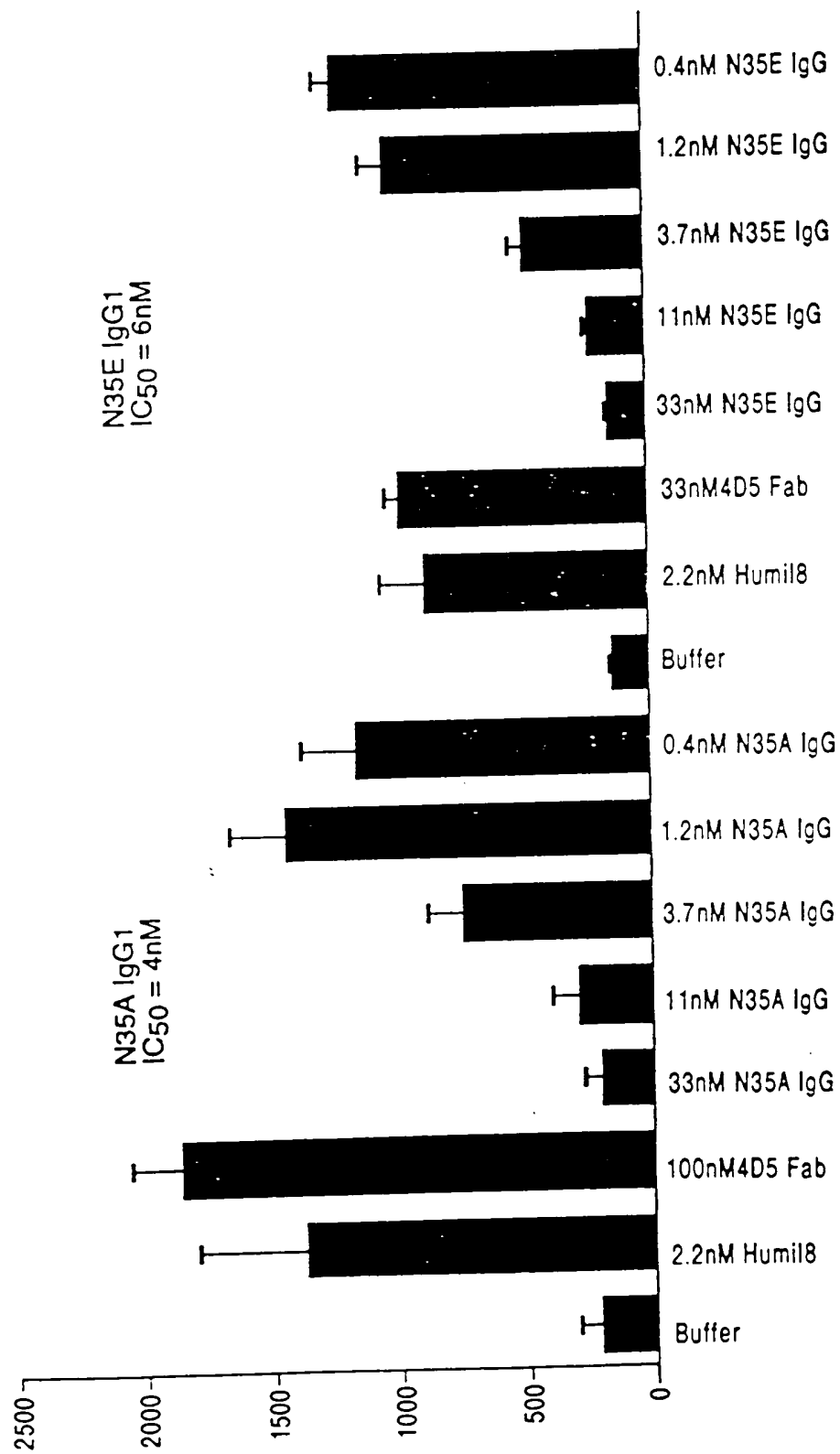


FIG. 50A

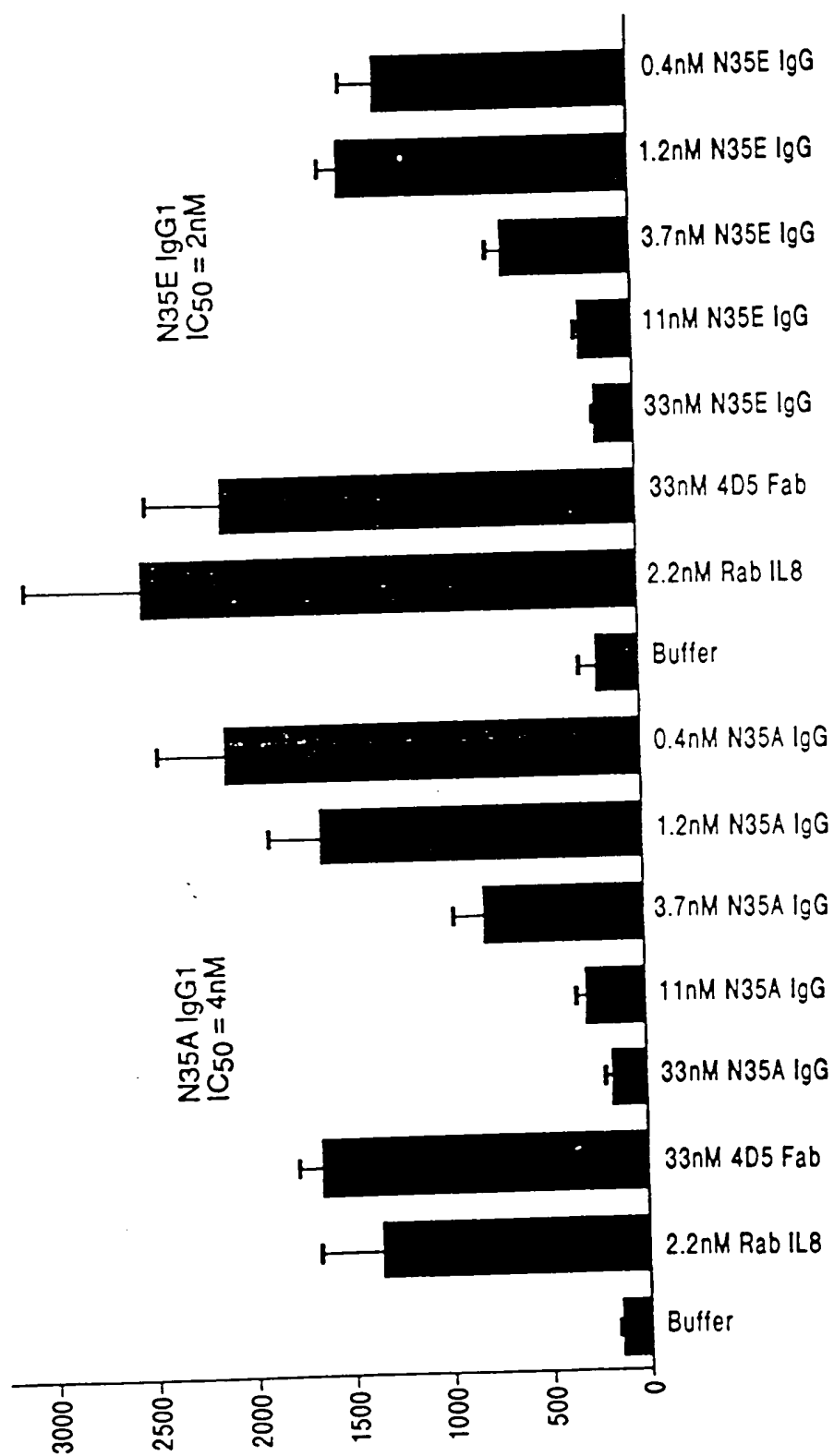
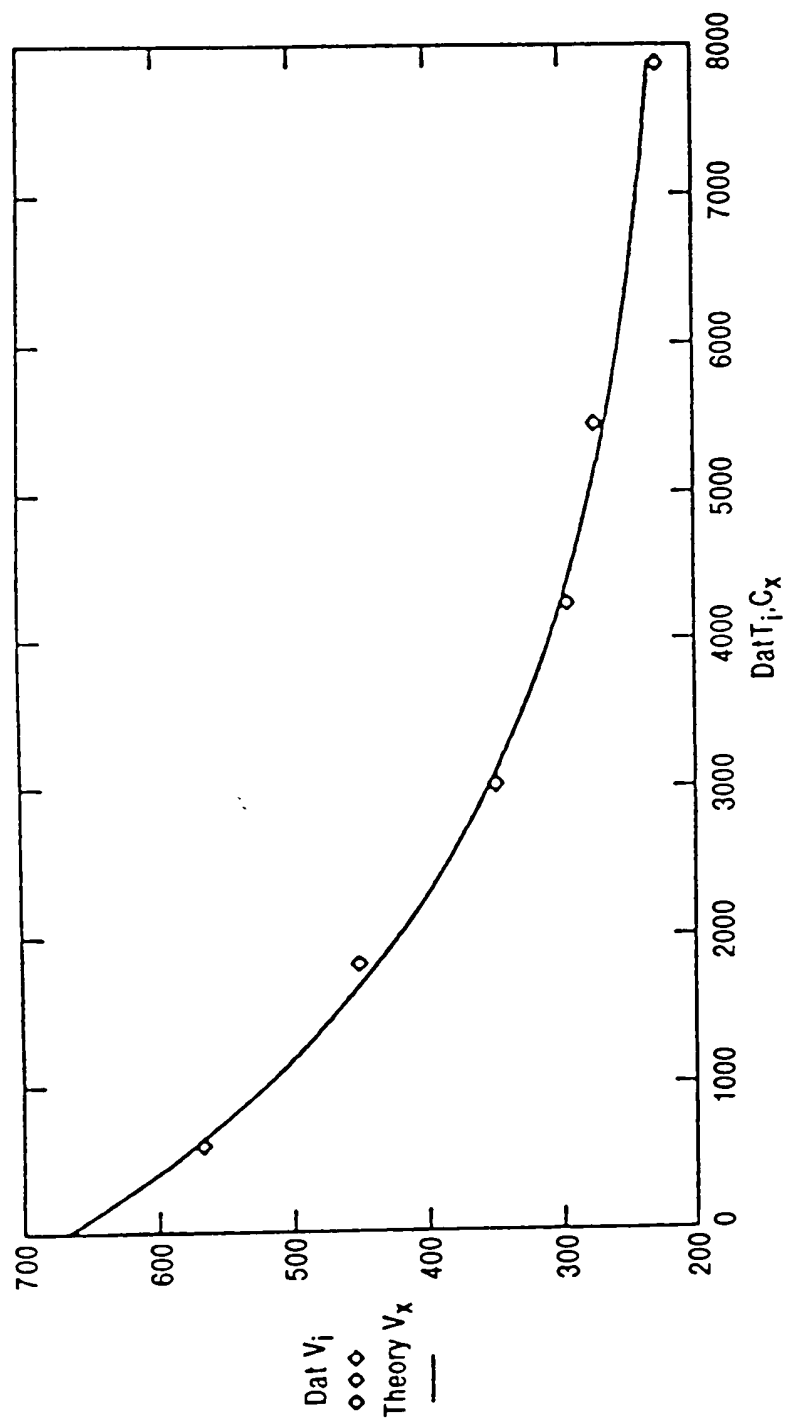


FIG. 50B



Representative Conc versus Time Plot. Shown is the kinetic data for 6G4V11N35A.IgG1

SAMPLE	k_a	k_d	K_d
Murine 6G4.2.5 IgG2a	8.3×10^5	2.9×10^{-4}	350pM
6G4V11N35A-IgG1	8.7×10^5	7.7×10^{-5}	88pM
6G4V11N35E-IgG1	3.0×10^6	1.4×10^{-4}	49pM

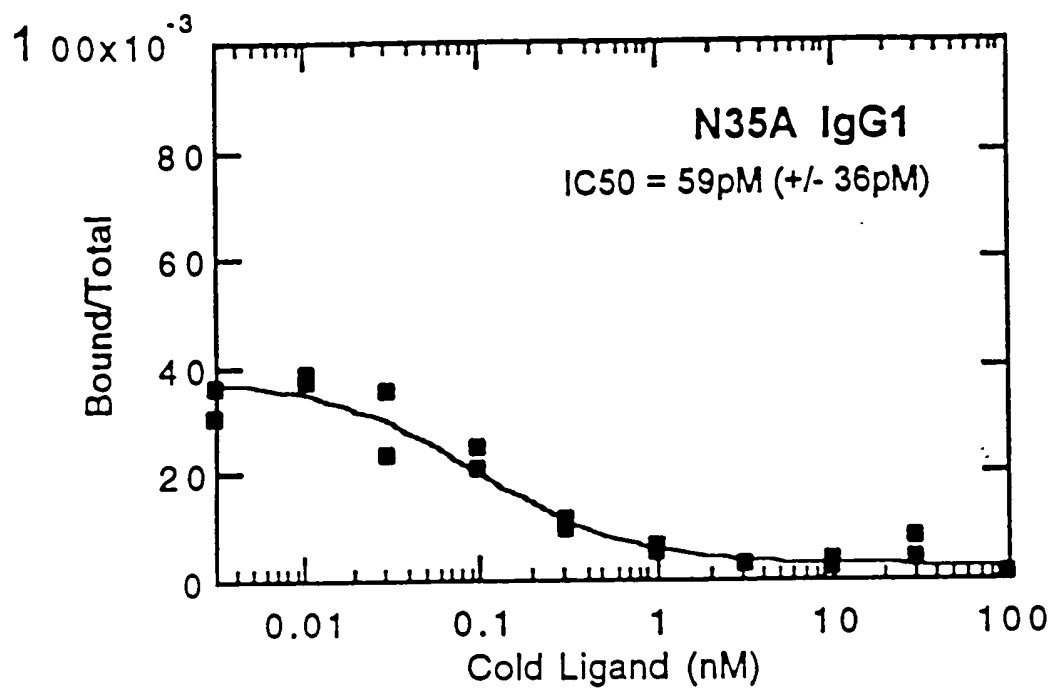


FIG. 52A

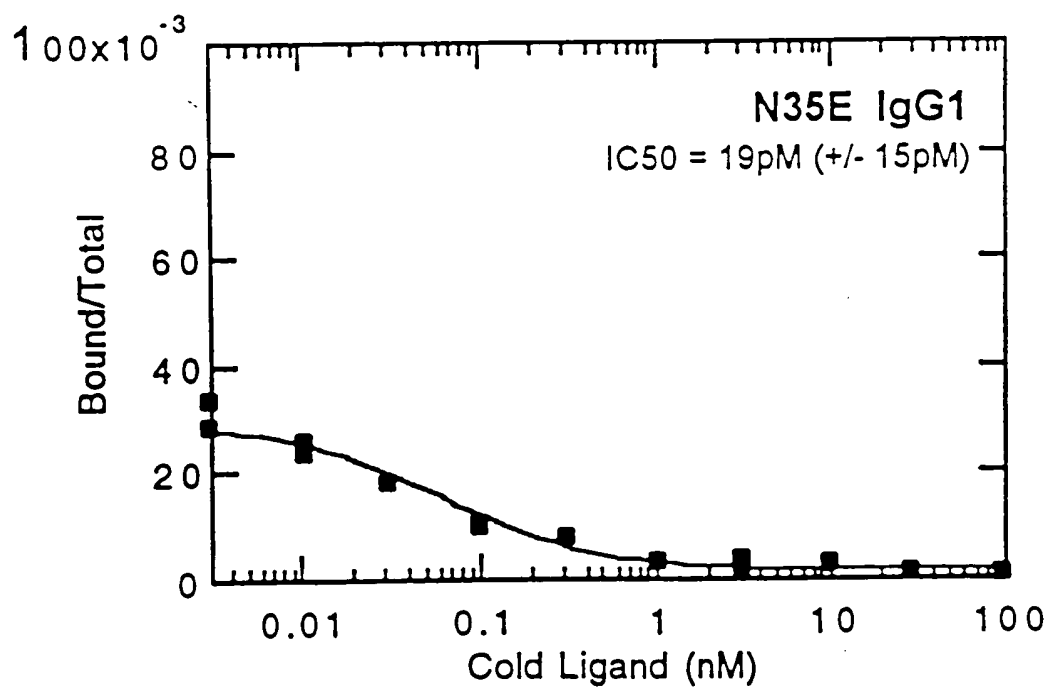


FIG. 52B

781 AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT TCTTCTTGCA
TTTTCCCATA GATCTCCAAC TCCACTAAAA TACTTTTTCT TATAGCGTAA AGAAGAACGT
-1 M K K N I A F L L A

841 TCTATGTTCTG TTTTTTCTAT TGCTACAAAC GCGTACGCTG AGGTTCAGCT AGTGCAGTCT
AGATACAAGC AAAAAAGATA ACGATGTTTG CGCATGCGAC TCCAAGTCGA TCACGTCAGA
-11 S M F V F S I A T N A Y A E V Q L V Q S

901 GGCGGTGGCC TGGTGCAGCC AGGGGGCTCA CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC
CCGCCACCGG ACCACGTCGG TCCCCCGAGT GAGGCAAACA GGACACGTCG AAGACCGATG
8 G G G L V Q P G G S L R L S C A A S G Y

961 TCCTTCTCGA GTCACTATAT GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG
AGGAAGAGCT CAGTGATATA CGTGACCCAG GCAGTCCGGG GCCCATTCCC GGACCTTACC
28 S F S S H Y M H W V R Q A P G K G L E W

1021 GTTGGATATA TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT
CAACCTATAT AACTAGGAAG GTTACCACTT TGATGCATAT TAGTTTTCAA GTTCCCGGCA
48 V G Y I D P S N G E T T Y N Q K F K G R

1081 TTCACTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA CAGCCTGCGT
AAGTGAAATA GAGCGCTGTT GAGGTTTTTG TGTCGTATGG ACGTCTACTT GTCGGACGCA
68 F T L S R D N S K N T A Y L Q M N S L R

1141 GCTGAGGACA CTGCCGTCTA TTA CTGTGCA AGAGGGGATT ATCGCTACAA TGGTGA CTGG
CGACTCCTGT GACGGCAGAT AATGACACGT TCTCCCTAA TAGCGATGTT ACCACTGACC
88 A E D T A V Y Y C A R G D Y R Y N G D W

1201 TTCTTCGACG TCTGGGGTCA AGGAACCCTG GTCACCGTCT CCTCGGCCTC CACCAAGGGC
AAGAAGCTGC AGACCCCAGT TCCTTGGGAC CAGTGGCAGA GGAGCCGGAG GTGGTTCCCC
108 F F D V W G Q G T L V T V S S A S T K G

1261 CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG
GGTAGCCAGA AGGGGGACCG TGGGAGGAGG TTCTCGTGGA GACCCCCGTG TCGCCGGGAC
128 P S V F P L A P S S K S T S G G T A A L

1321 GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC
CCGACGGACC AGTTCCTGAT GAAGGGGCTT GGCCACTGCC ACAGCACCTT GAGTCCGCGG
148 G C L V K D Y F P E P V T V S W N S G A

1381 CTGACCAGCG GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTA CTCCCTC
GACTGGTCGC CGCACGTGTG GAAGGGCCGA CAGGATGTCA GGAGTCTGA GATGAGGGAG
168 L T S G V H T F P A V L Q S S G L Y S L

1441 AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG
TCGTGCGACC ACTGGCACGG GAGGTGCTCG AACCCGTGGG TCTGGATGTA GACGTTGCAC
188 S S V V T V P S S S L G T Q T Y I C N V

1501 AATCACAAGC CCAGCAACAC CAAGGTCGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA
TTAGTGTTCTG GGTGCTGTG GTTCCAGCTG TTCTTTCAAC TCGGGTTTAG AACACTGTTT
208 N H K P S N T K V D K K V E P K S C D K

1561 ACTCACACAT GCCCGCCGTGA (SEQ ID NO: 69)
TGAGTGTGTA CGGGCGGCACT
228 T H T C P P O
(SEQ ID NO: 70)

FIG. 53

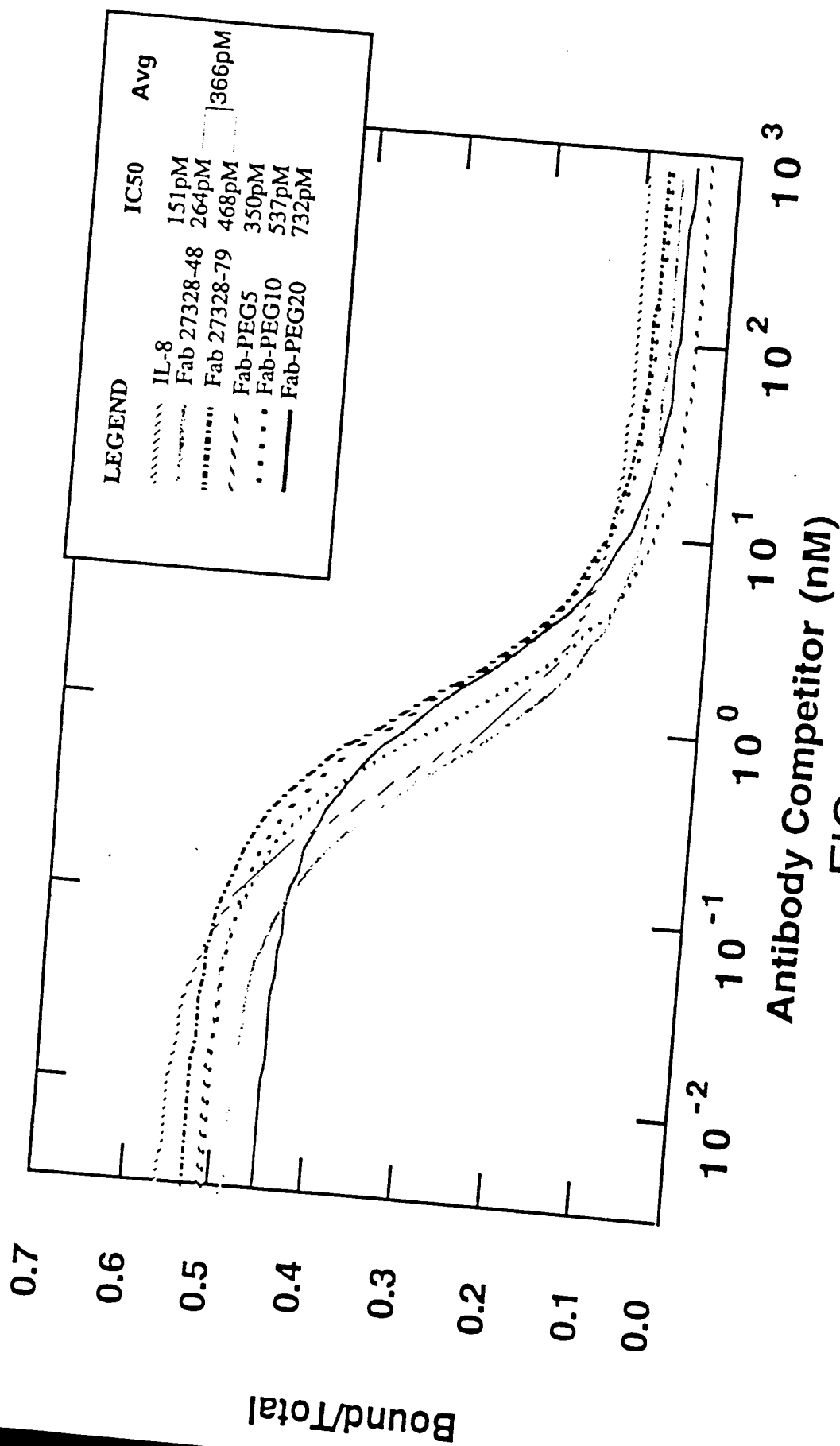


FIG. 54A

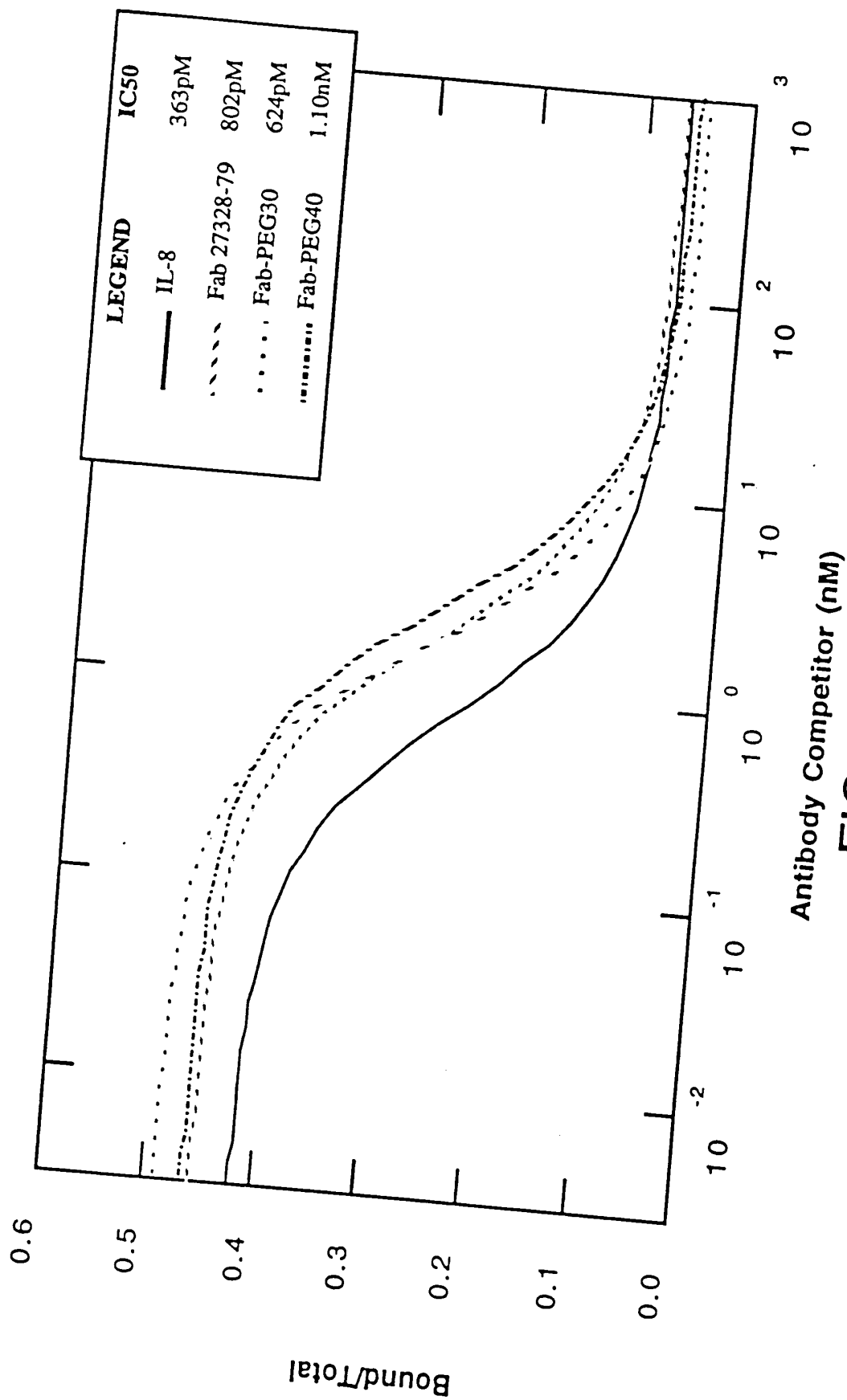
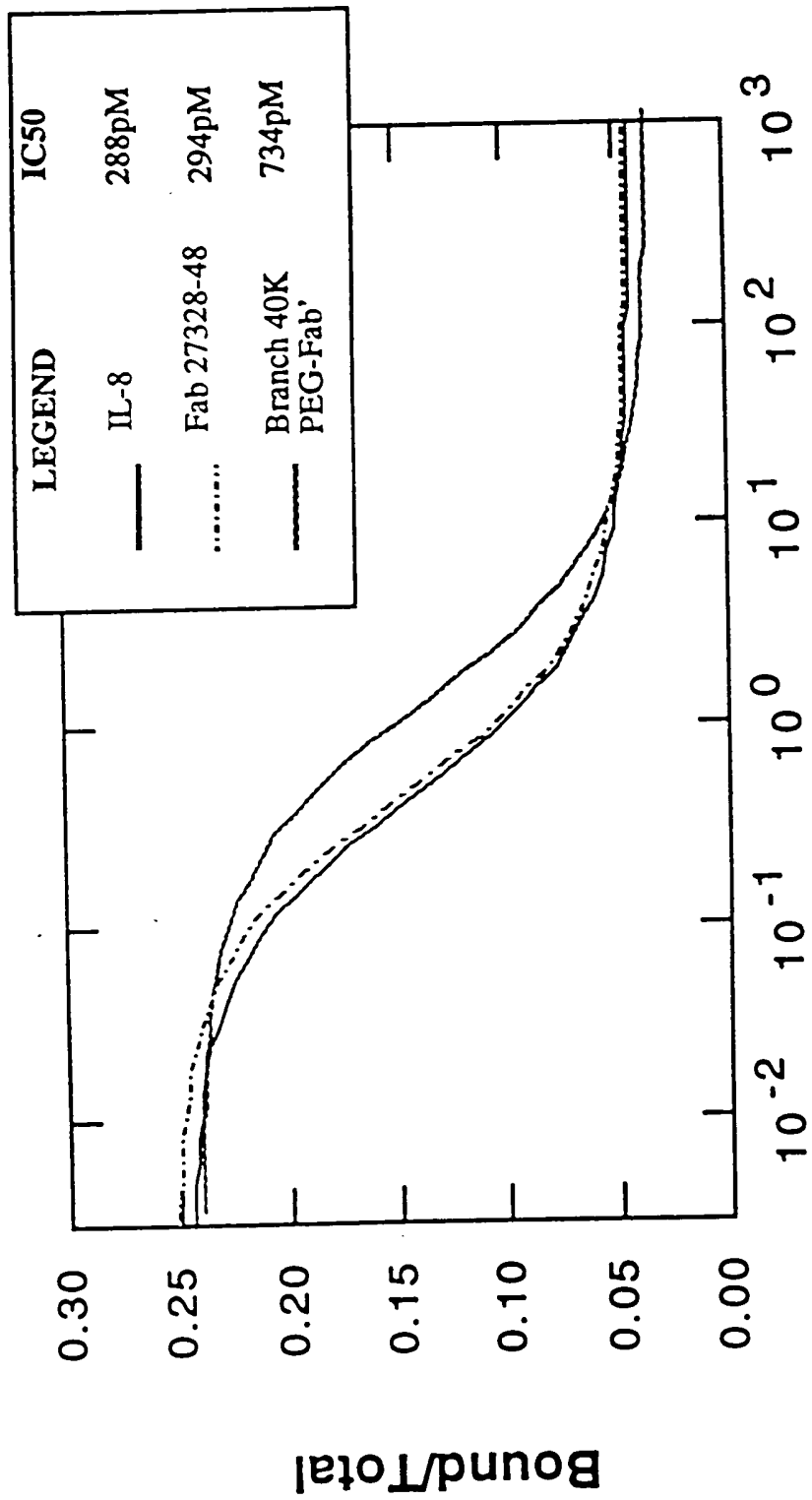


FIG. 54B



Antibody Competitor (nM)

FIG. 54C

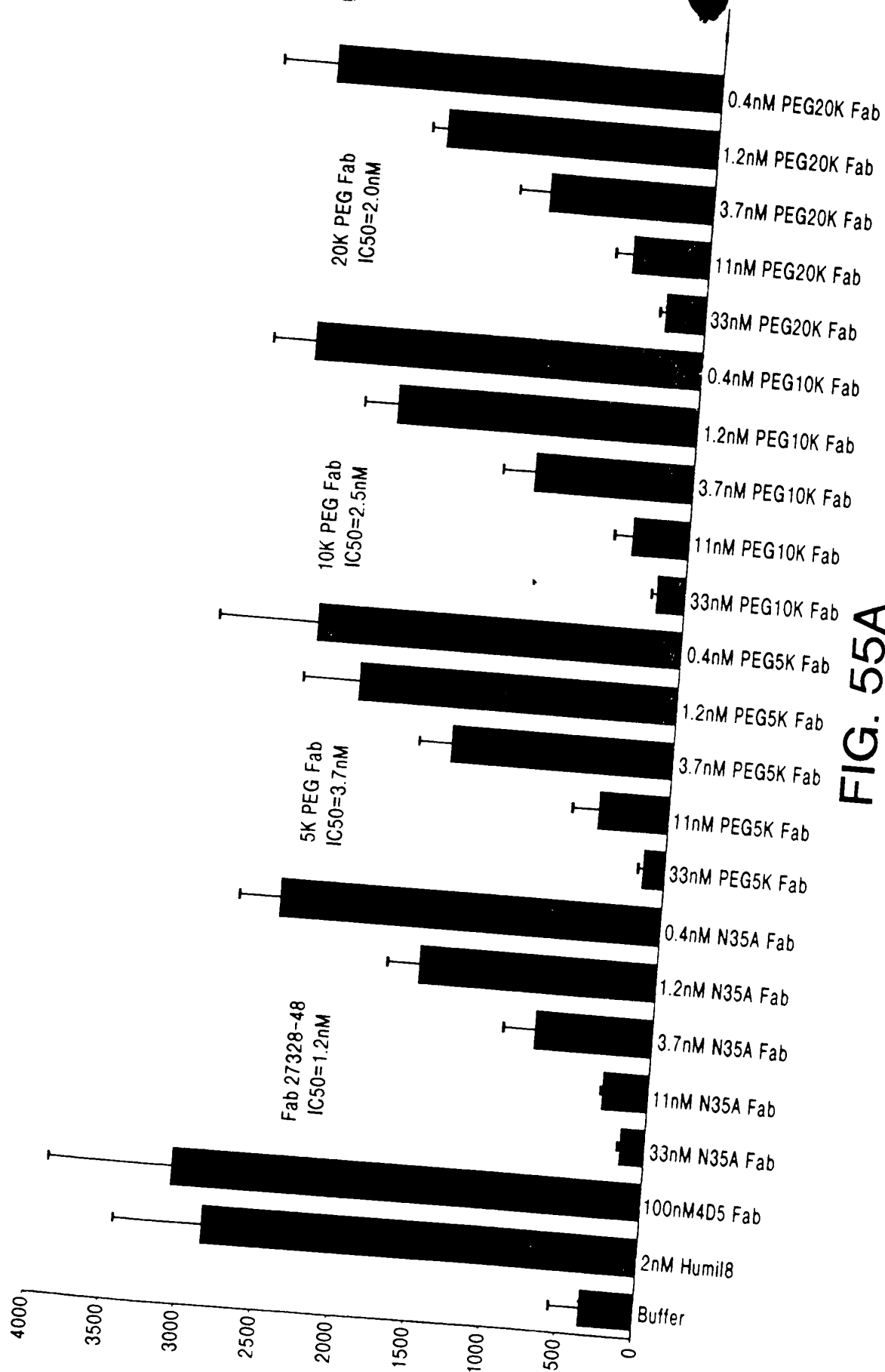


FIG. 55A

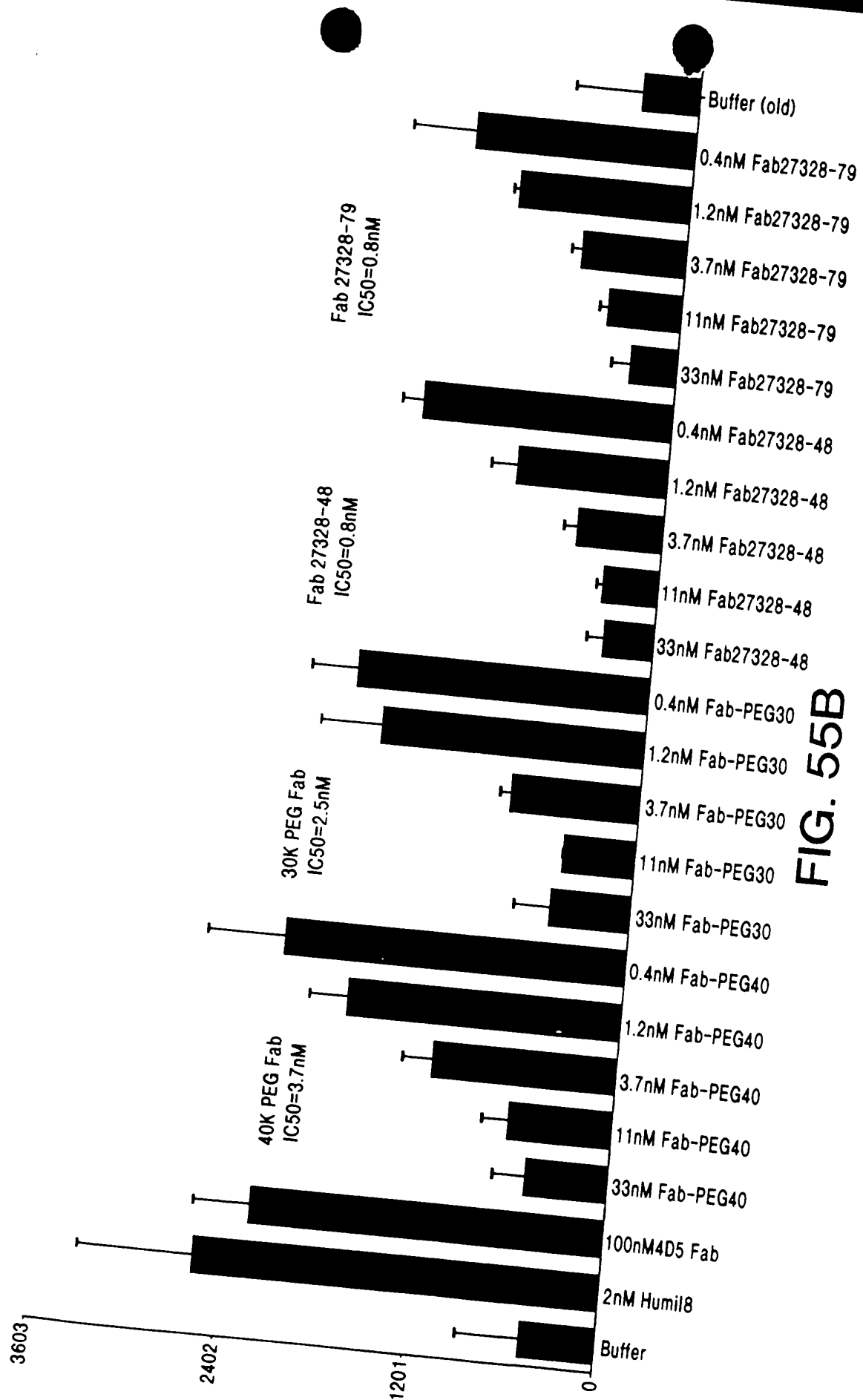


FIG. 55B

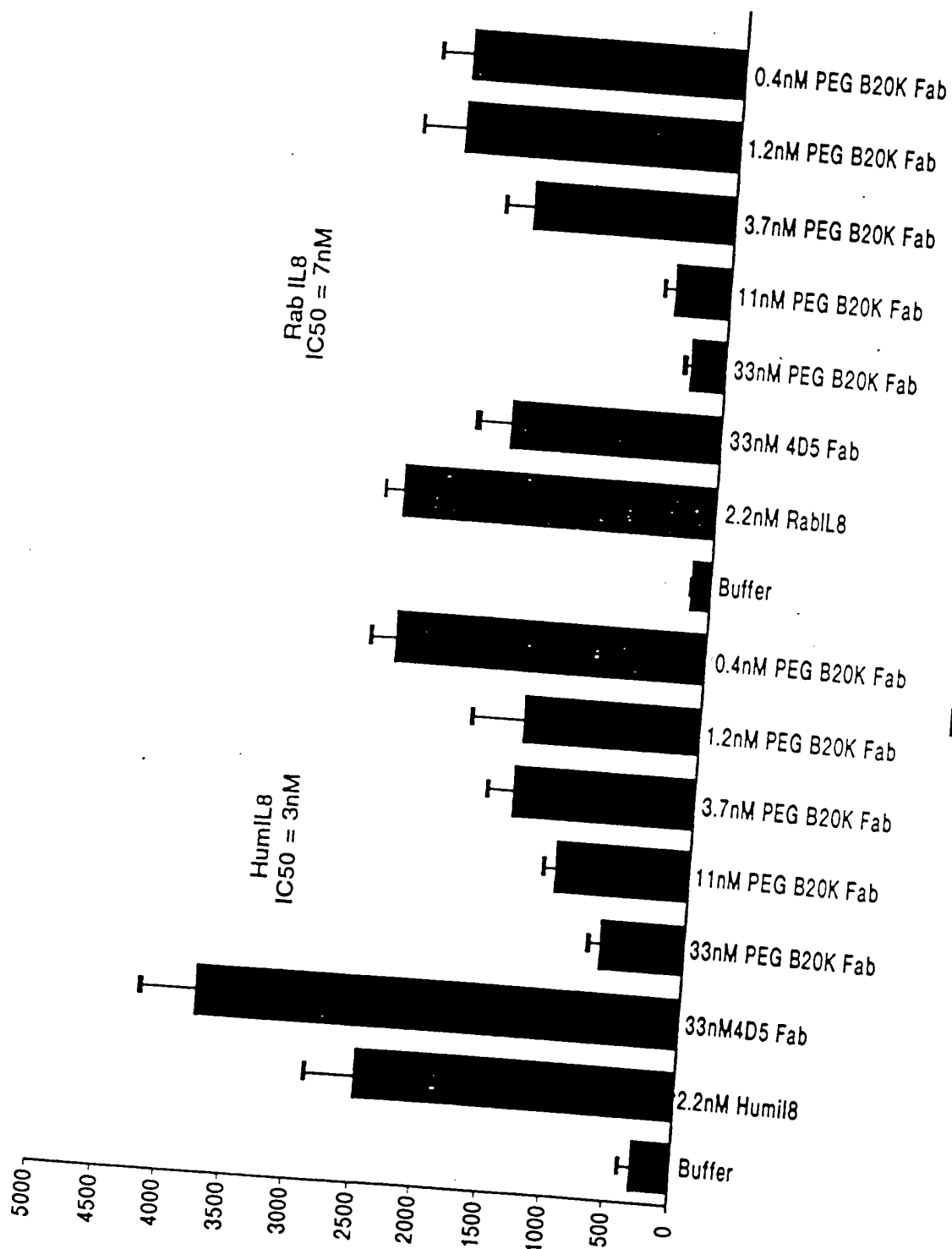
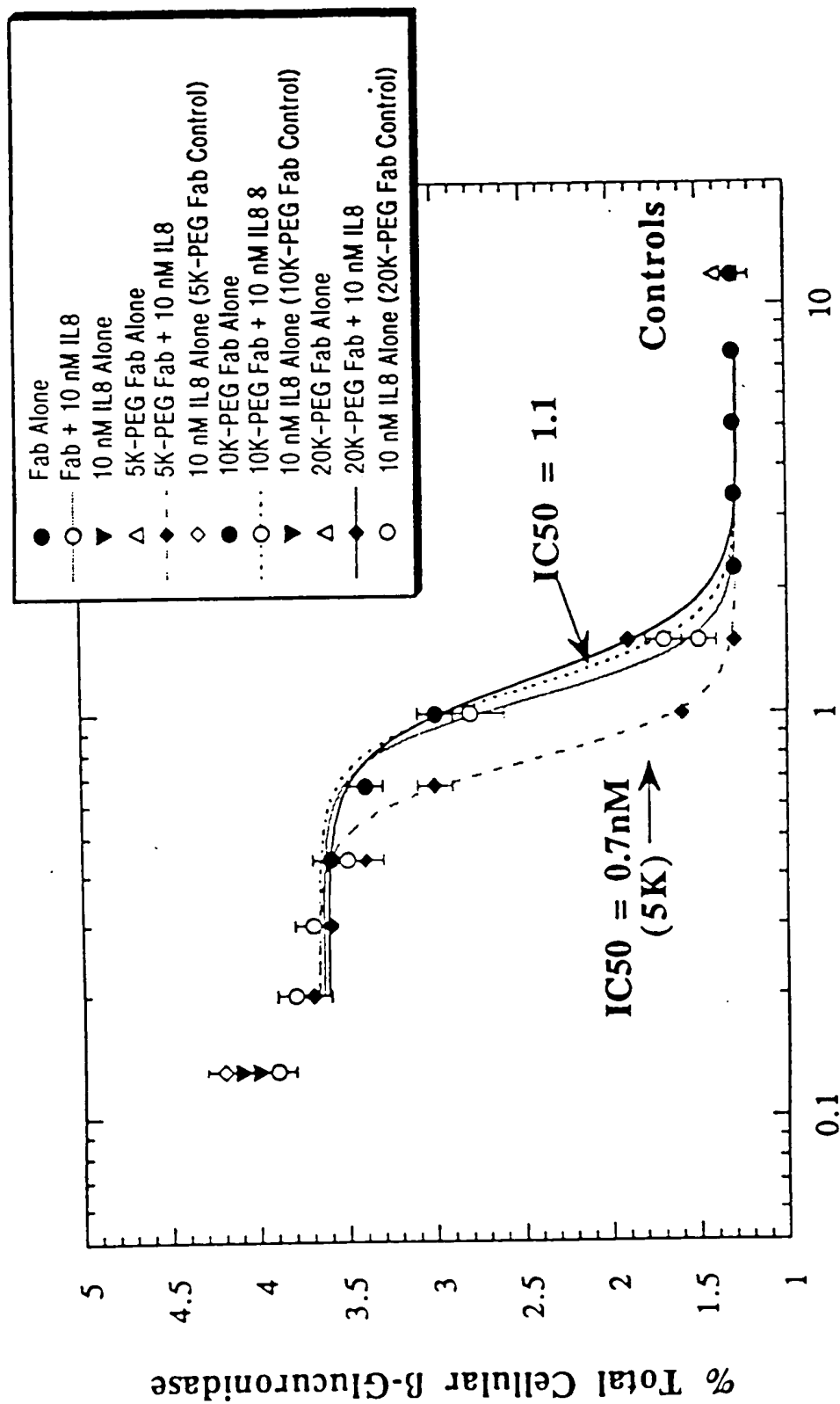


FIG. 55C



Molar Ratio Antibody:IL-8

FIG. 56A

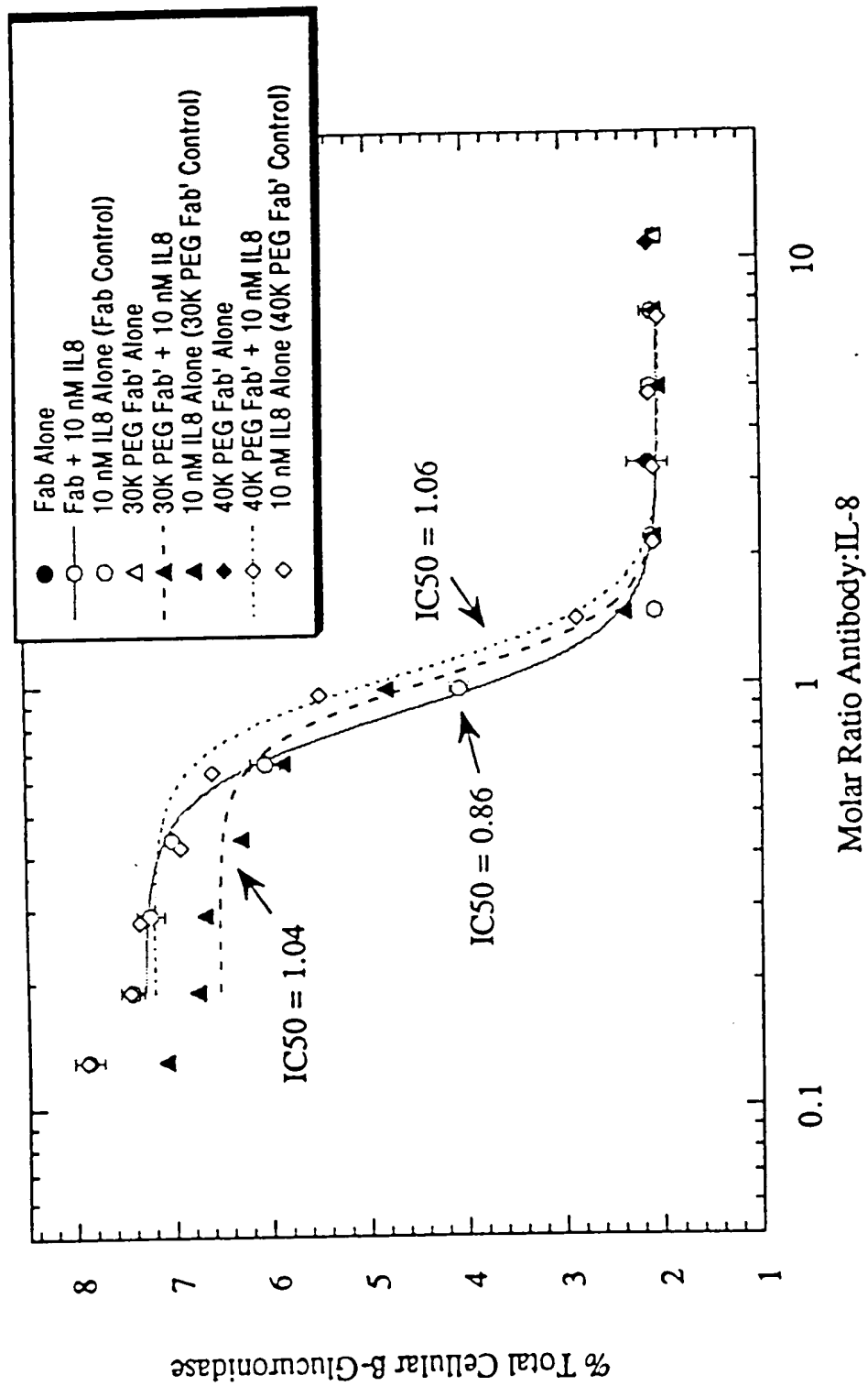
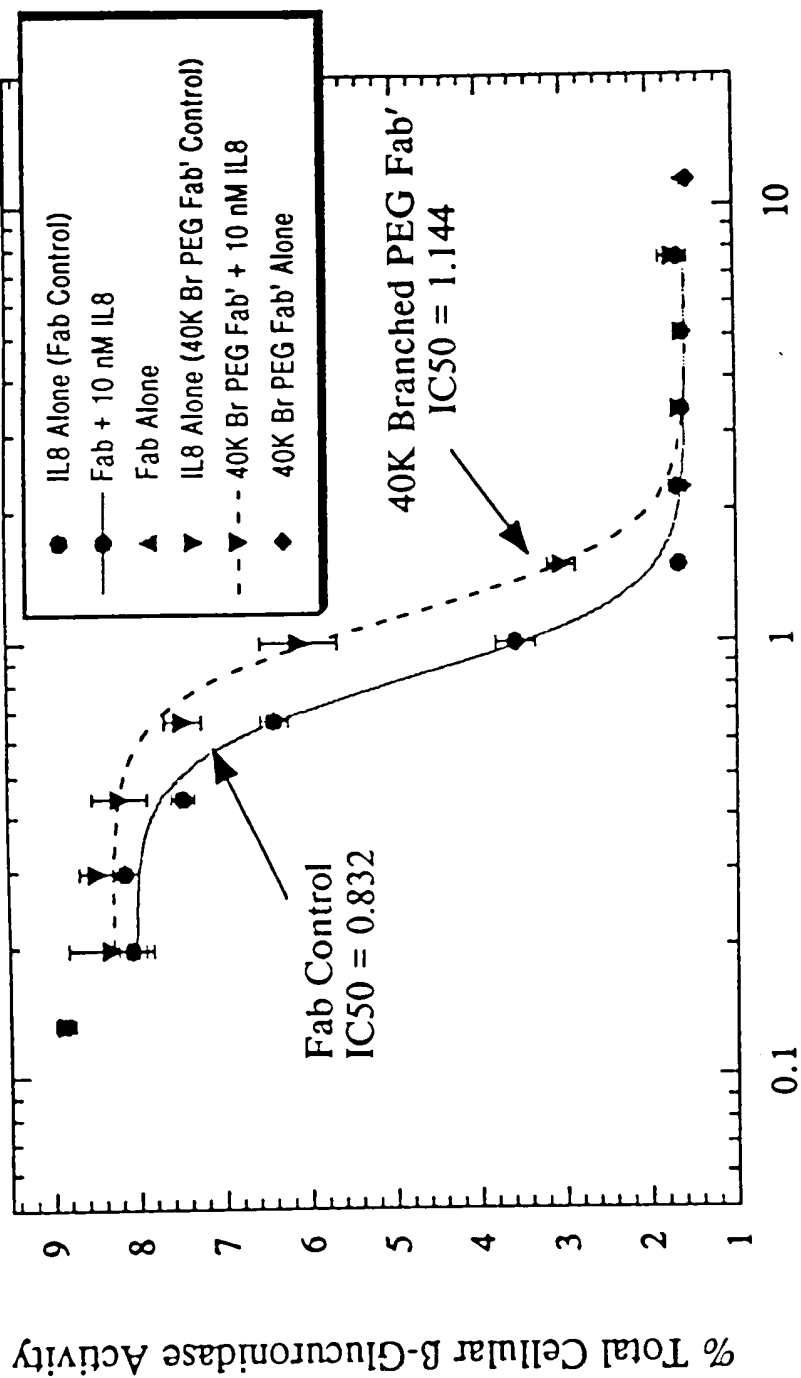
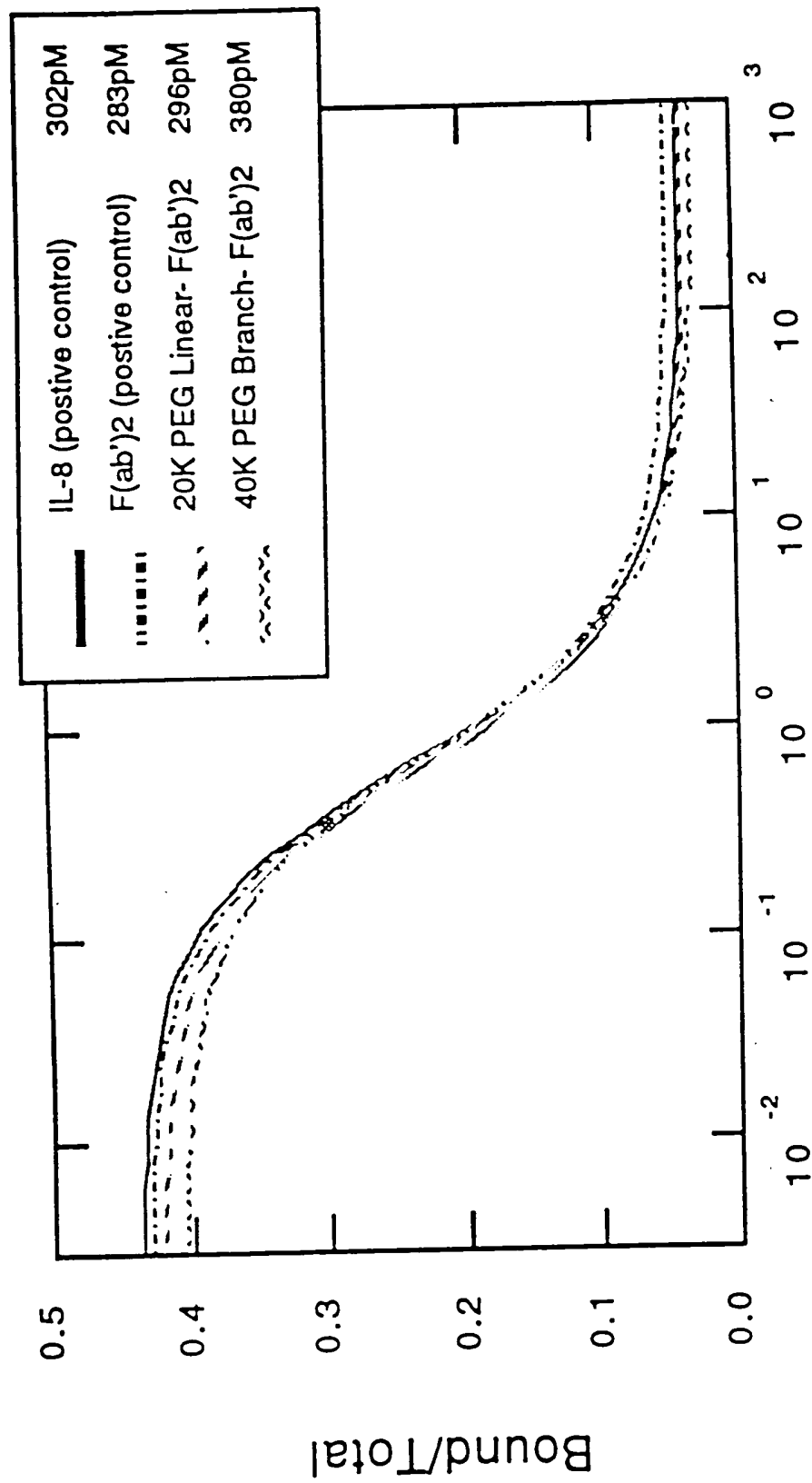


FIG. 56B



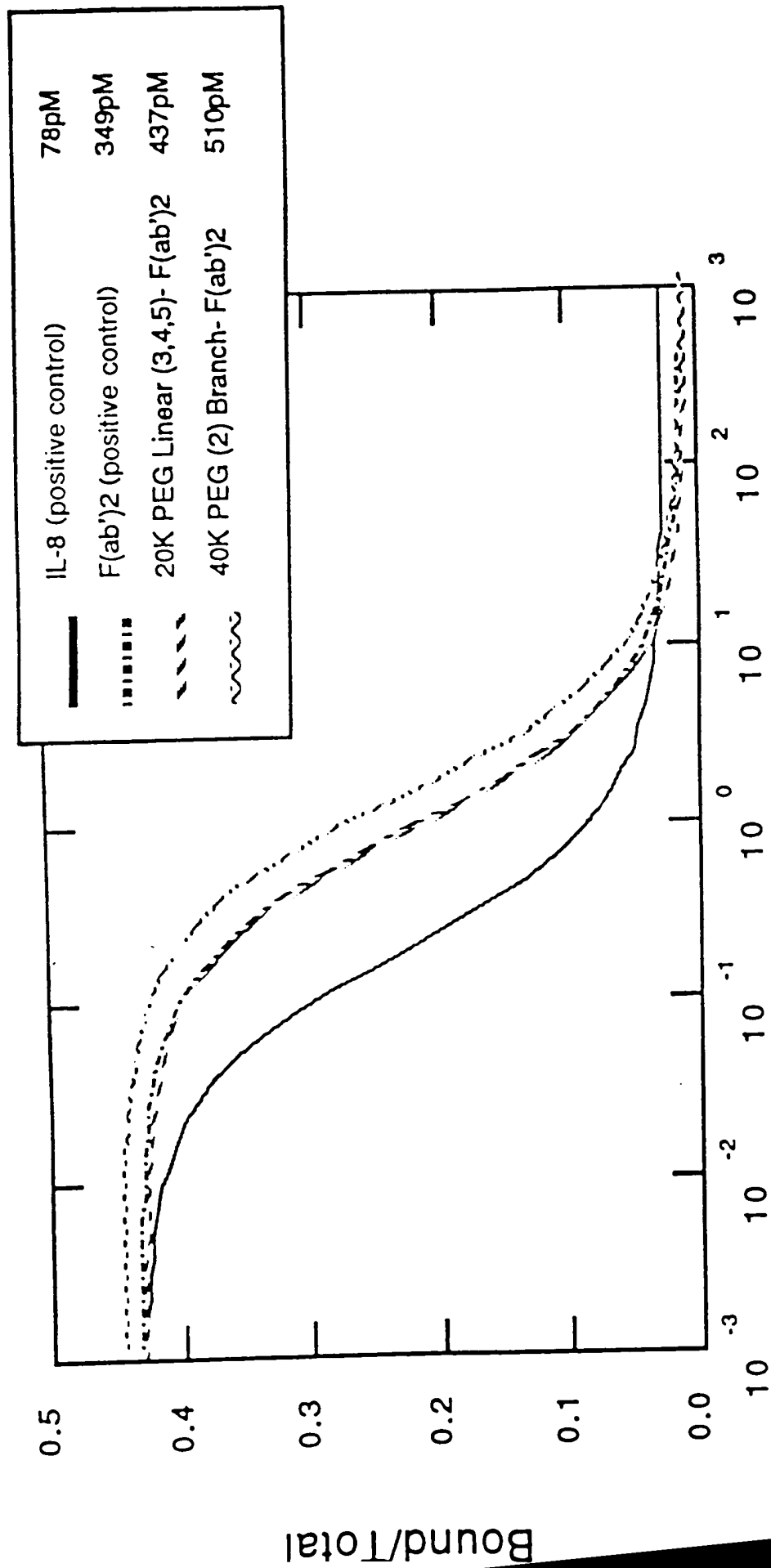
Molar Ratio Antibody:IL8

FIG. 56C



Pegylated F(ab')₂ (nM)

FIG. 57A



Pegylated F(ab')₂ (nM)

FIG. 57B

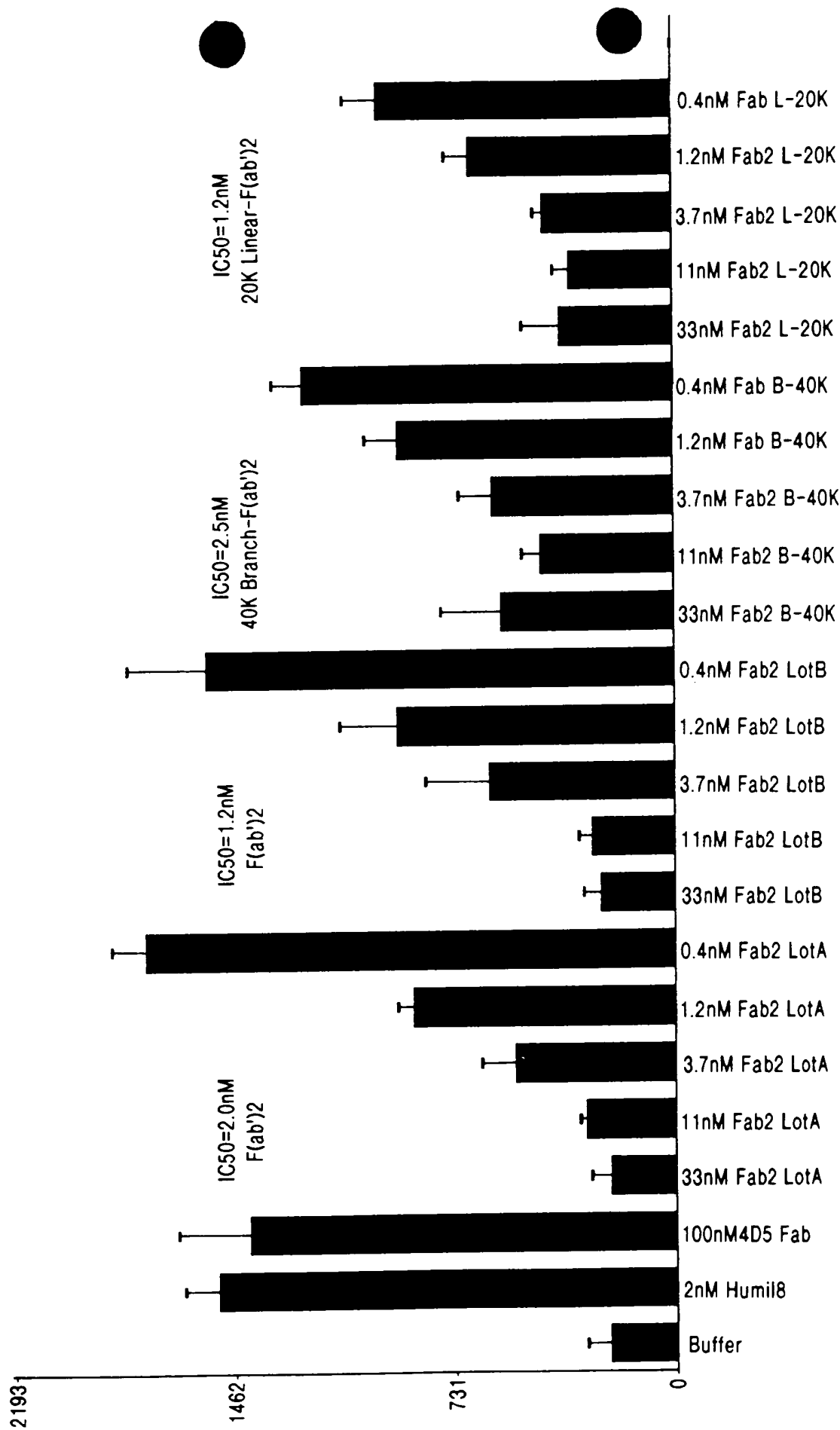


FIG. 58A

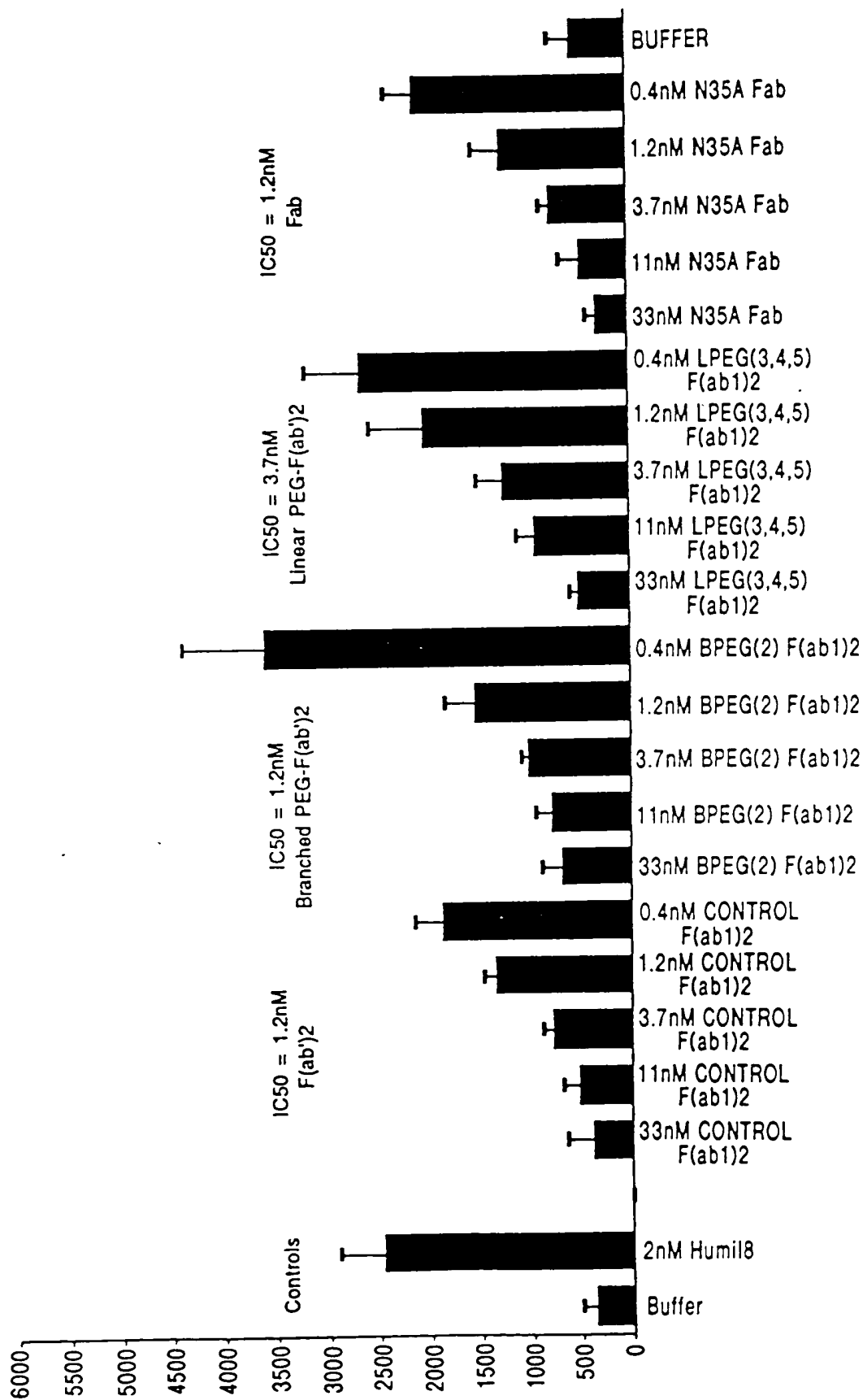


FIG. 58B

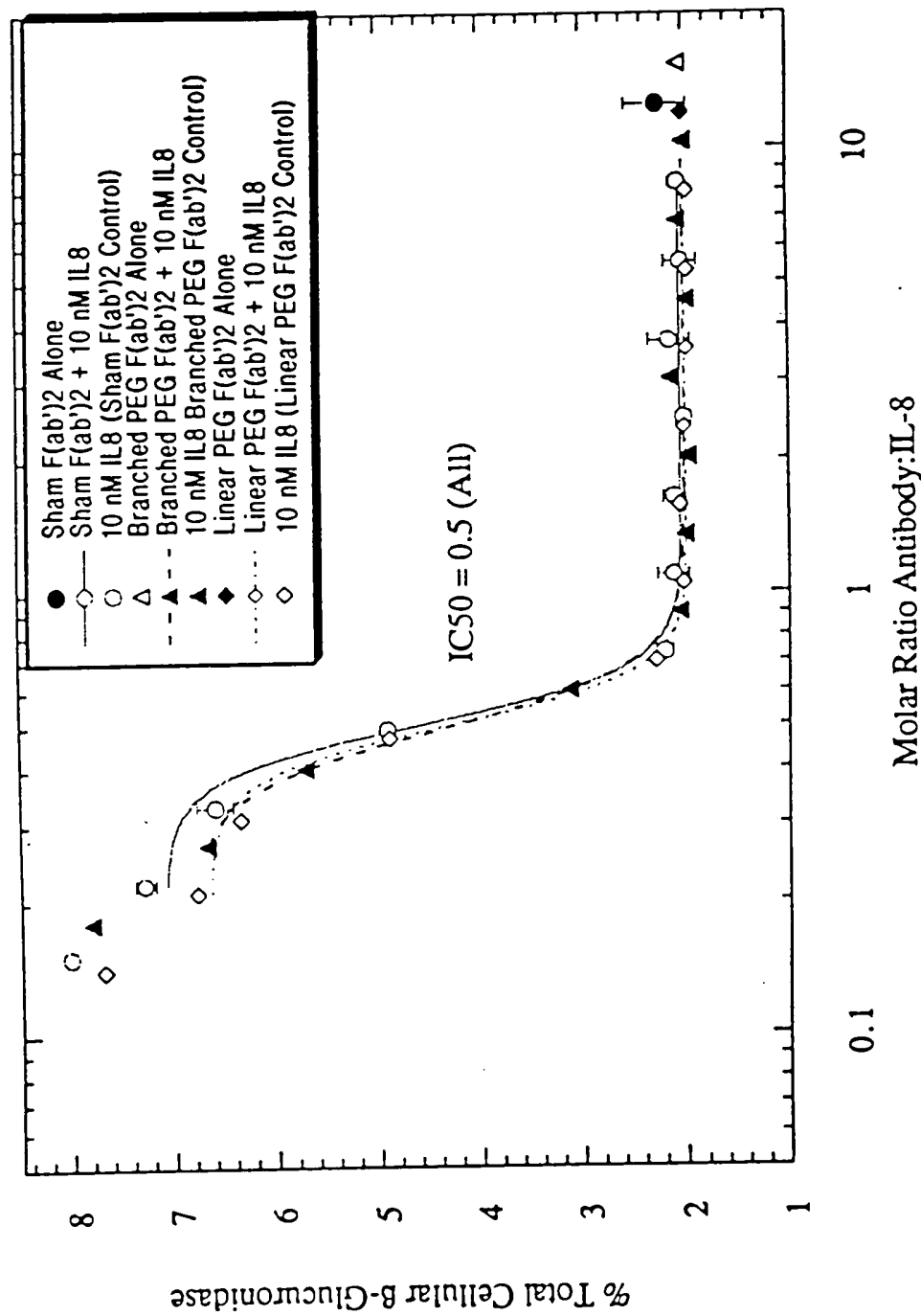
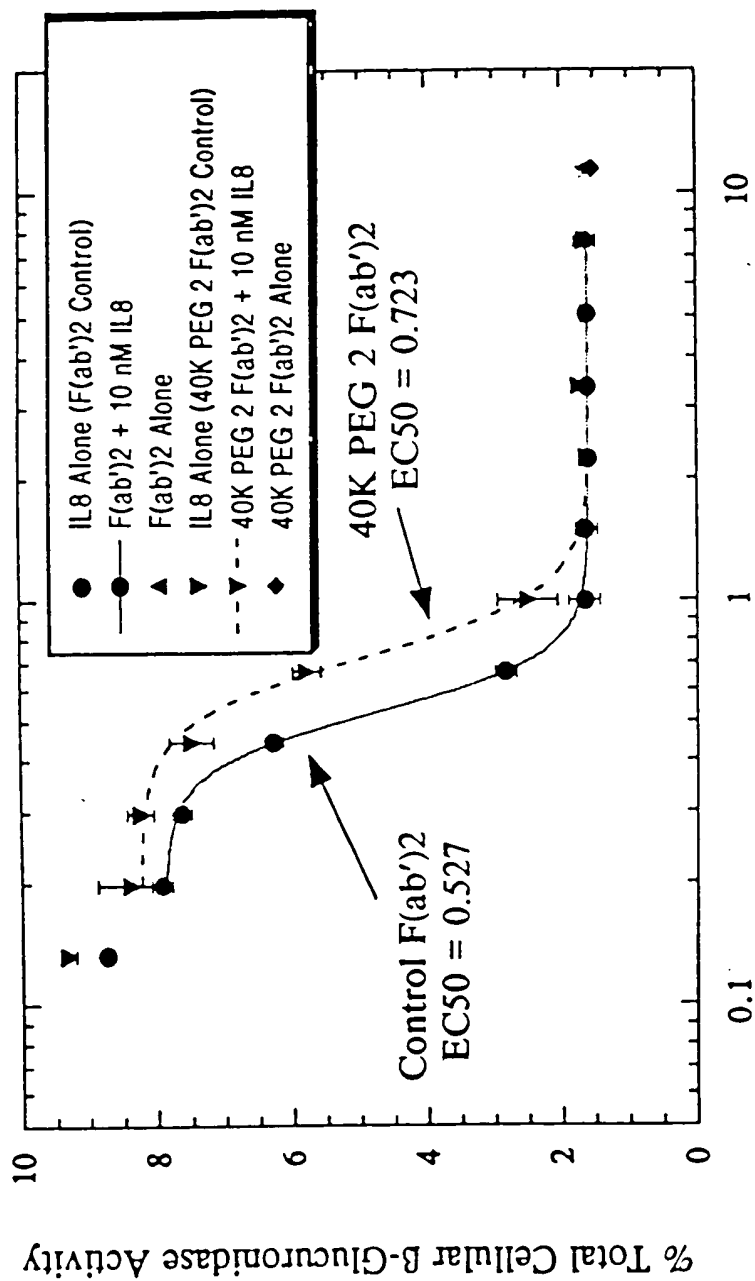


FIG. 59A



Molar Ratio Antibody:IL8

FIG. 59B

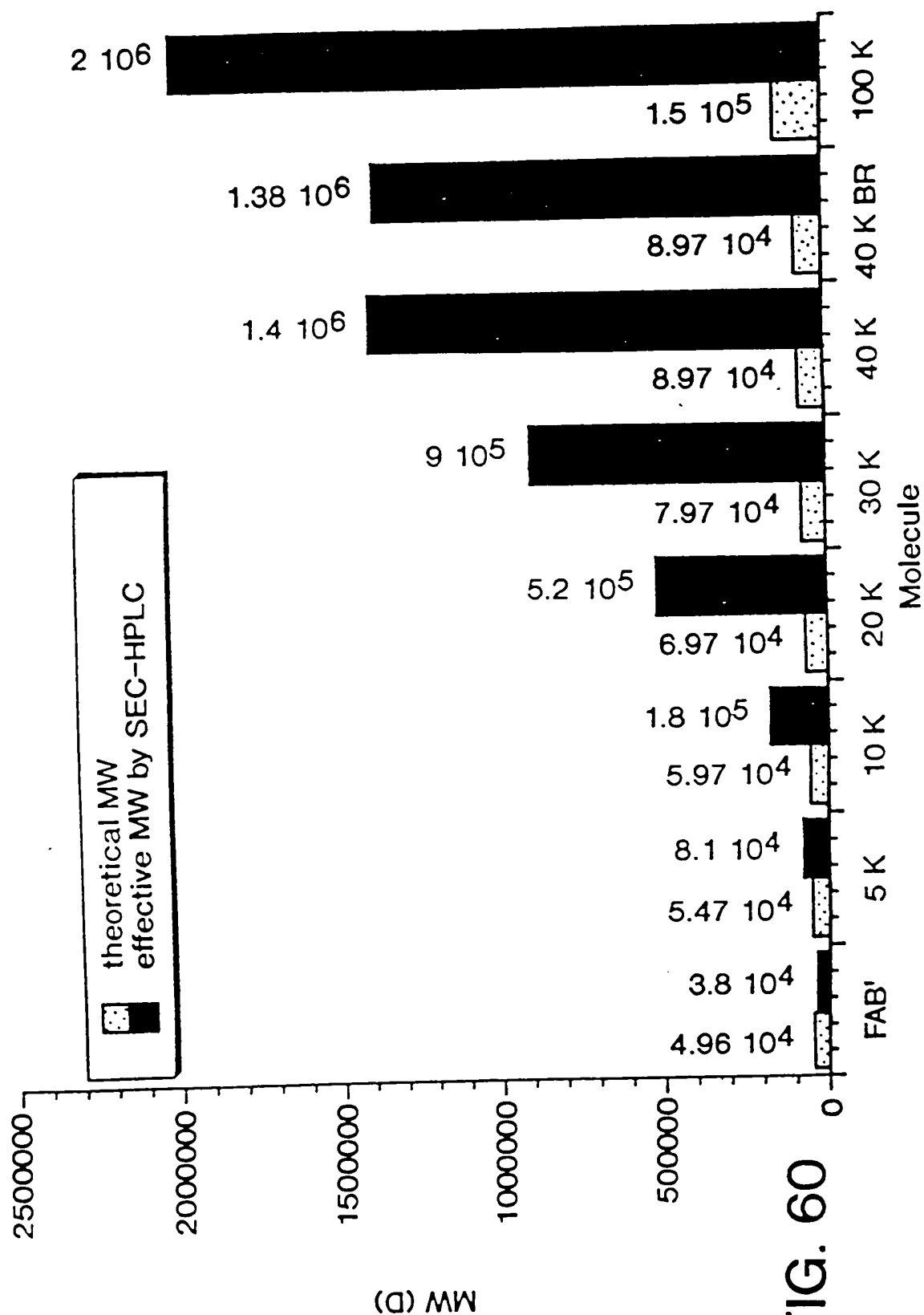
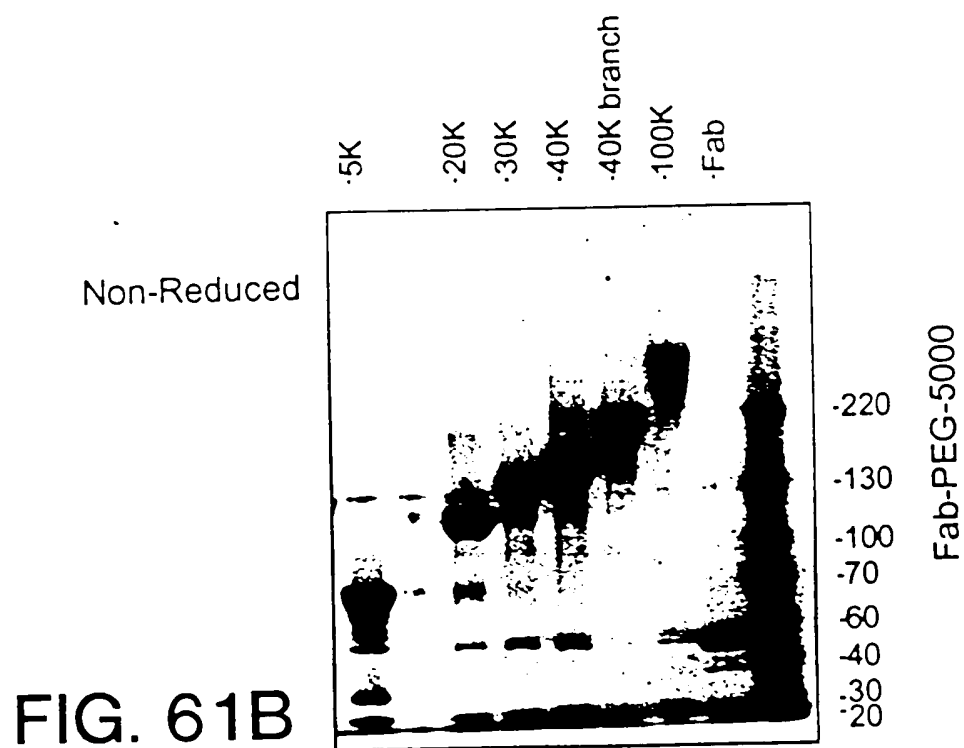
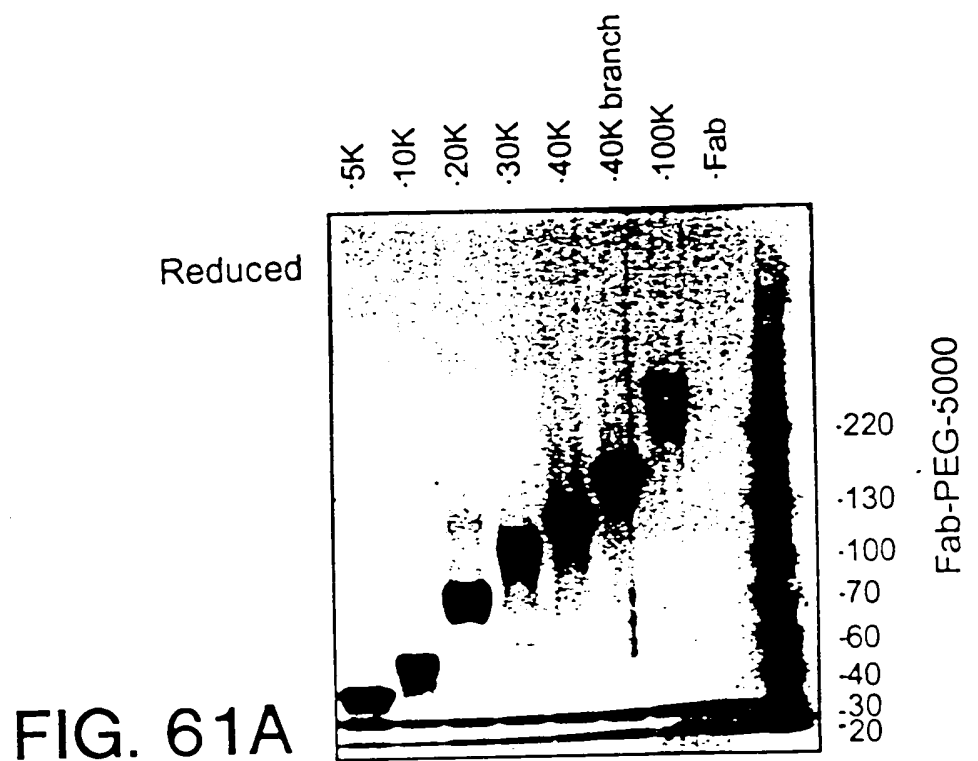


FIG. 60



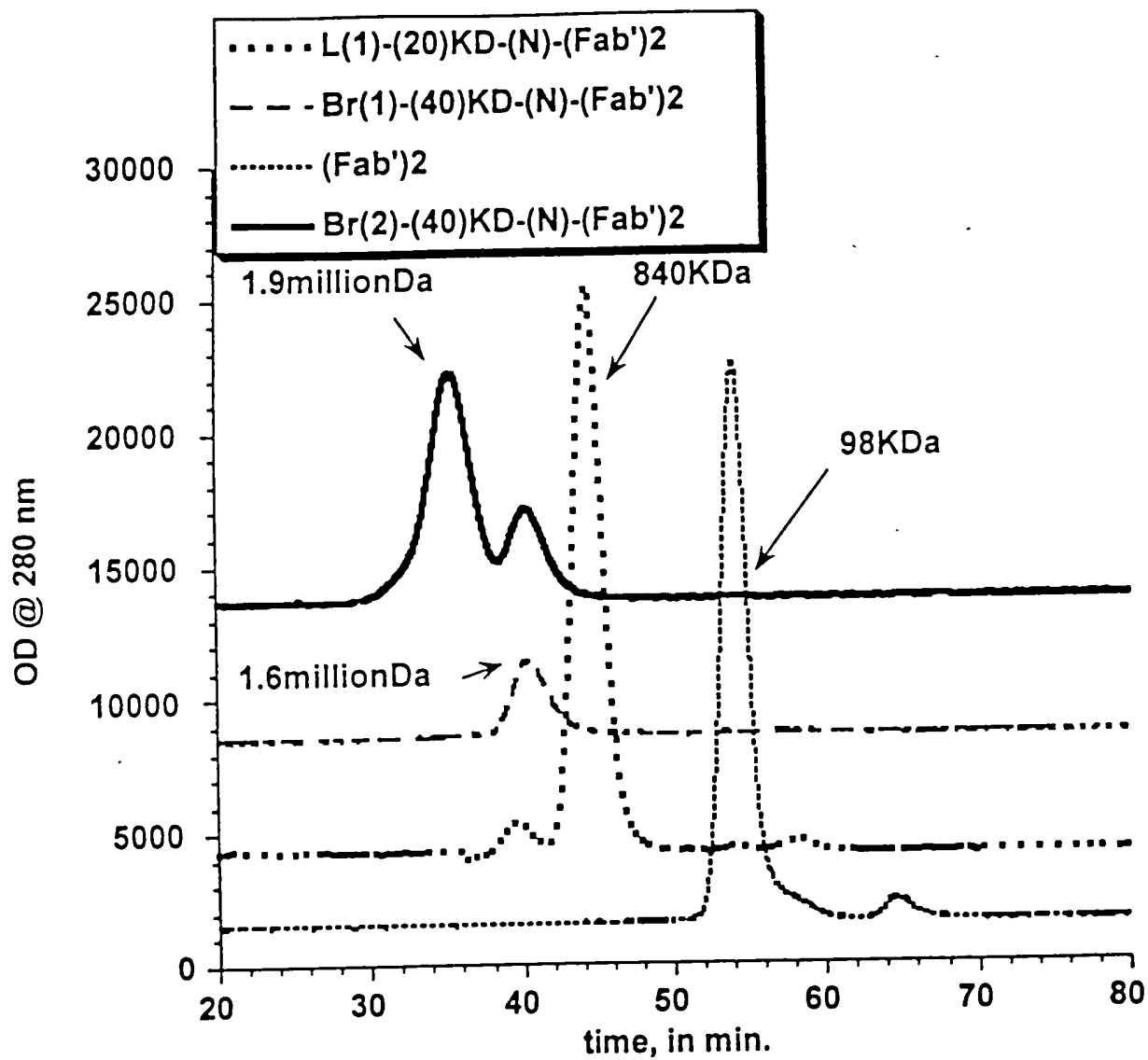


FIG. 62

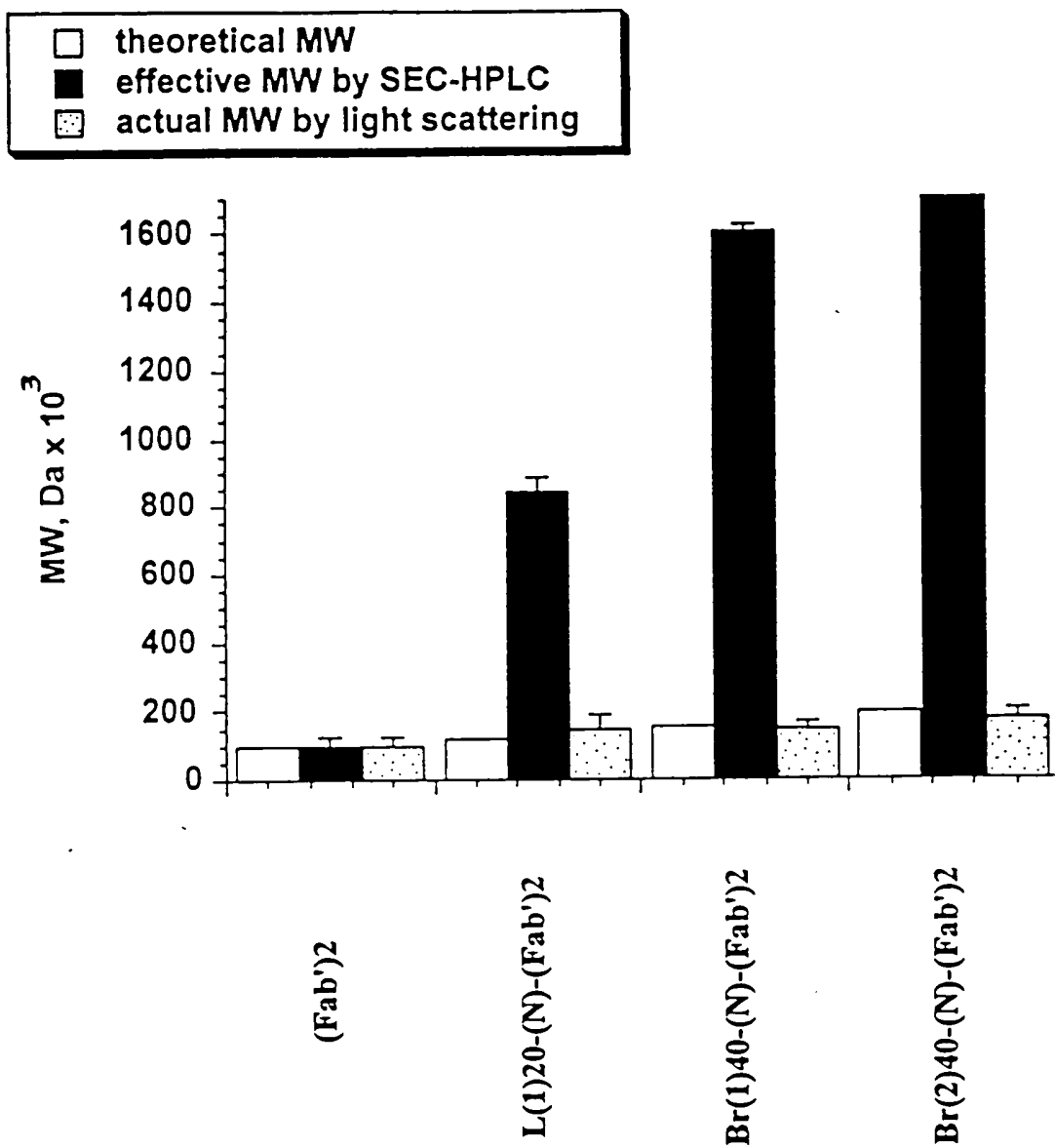


FIG. 63

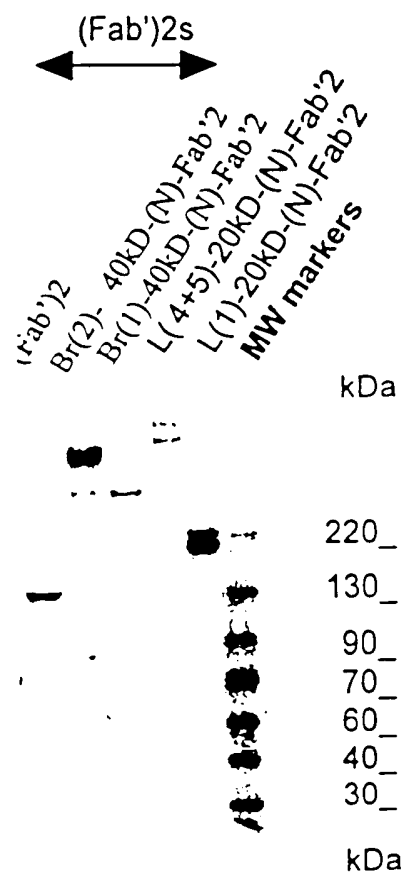
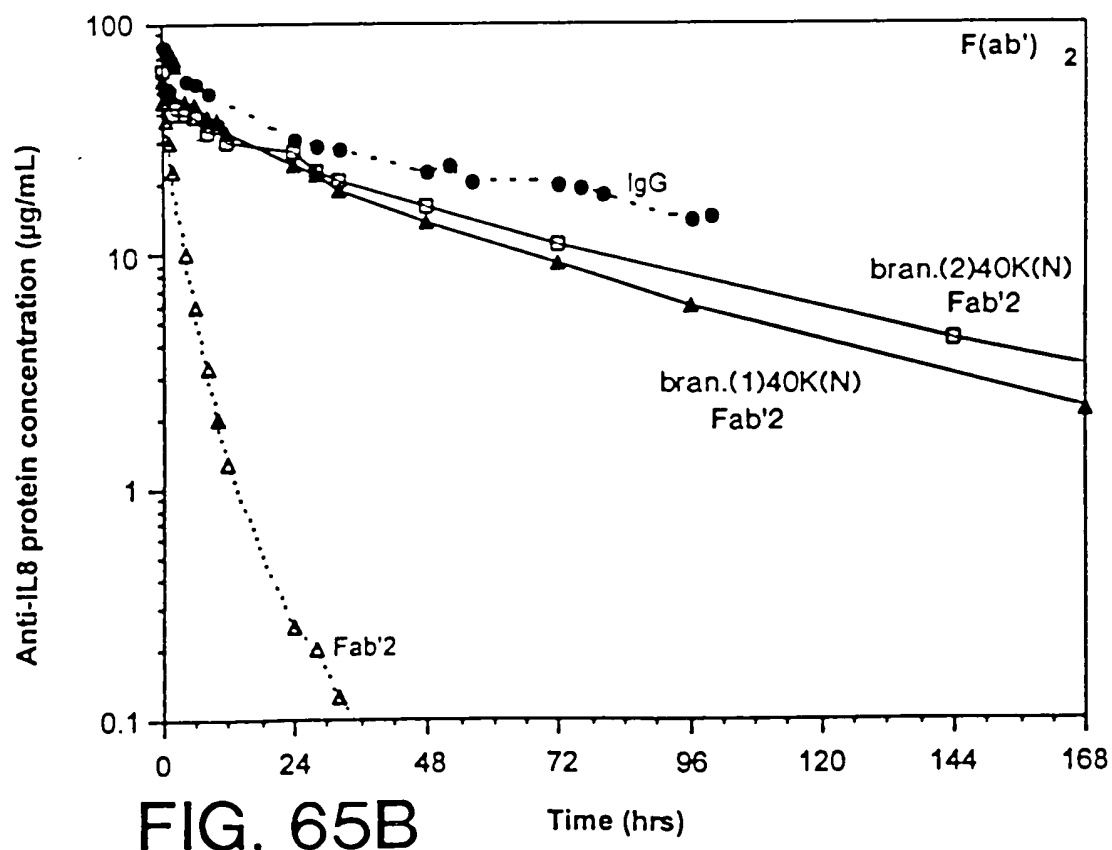
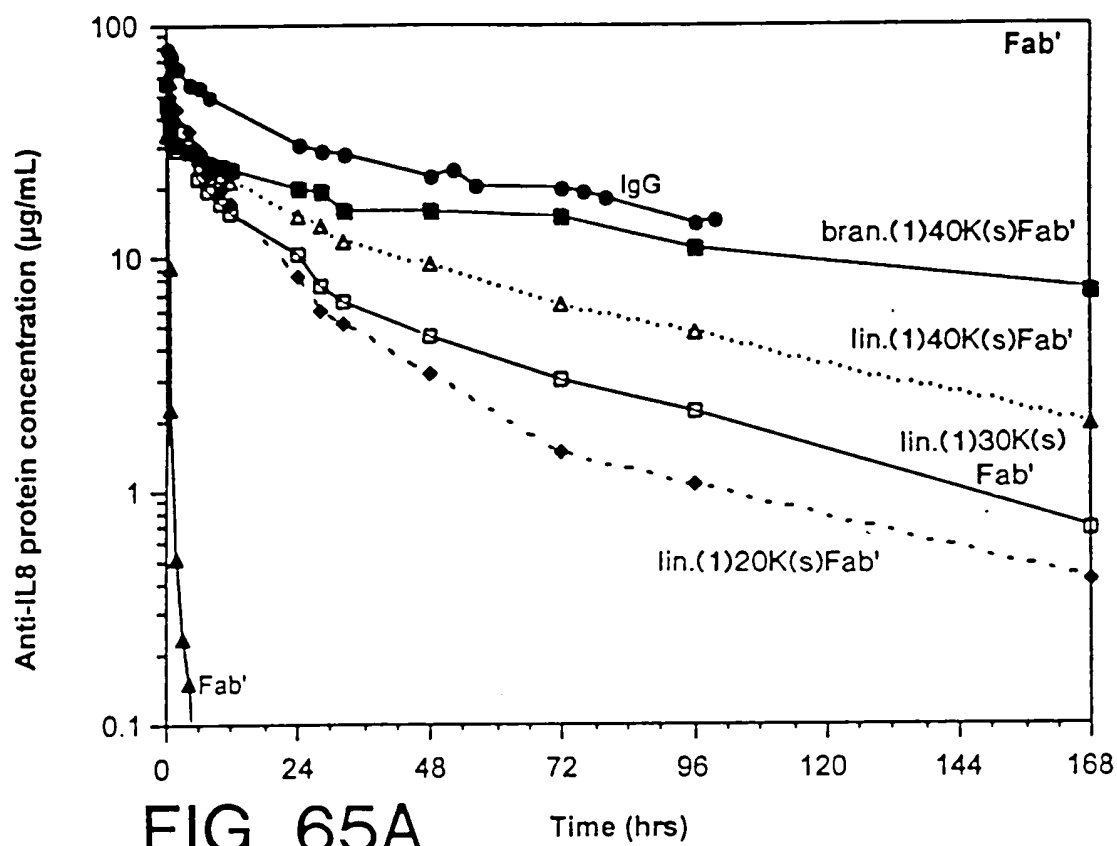


FIG. 64



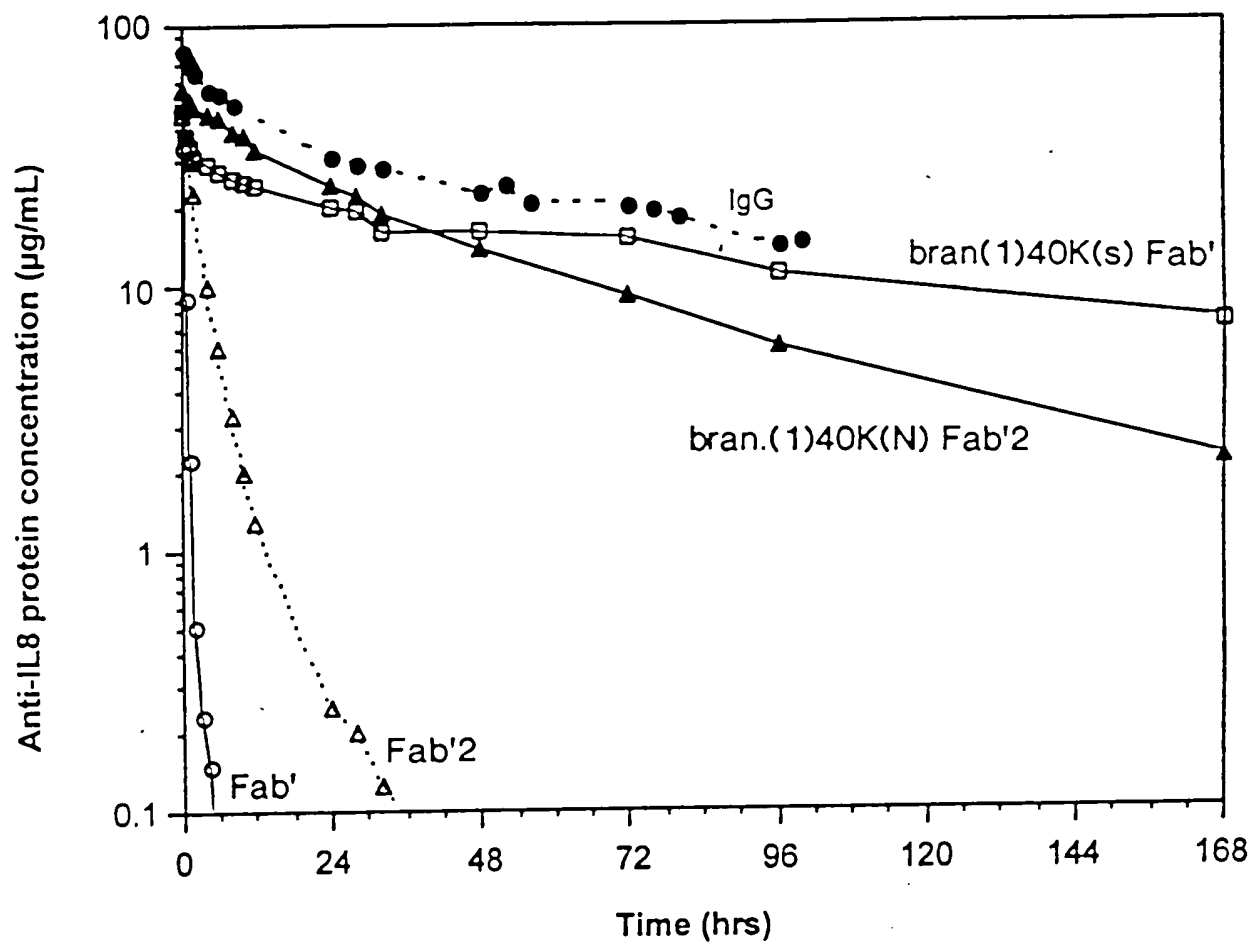


FIG. 66

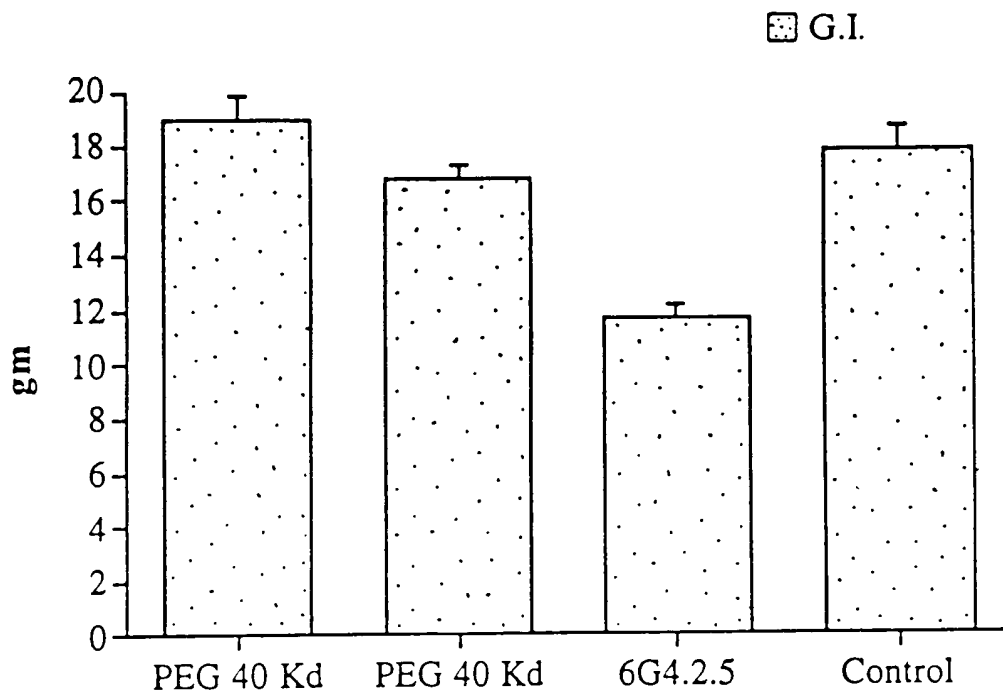


FIG. 67

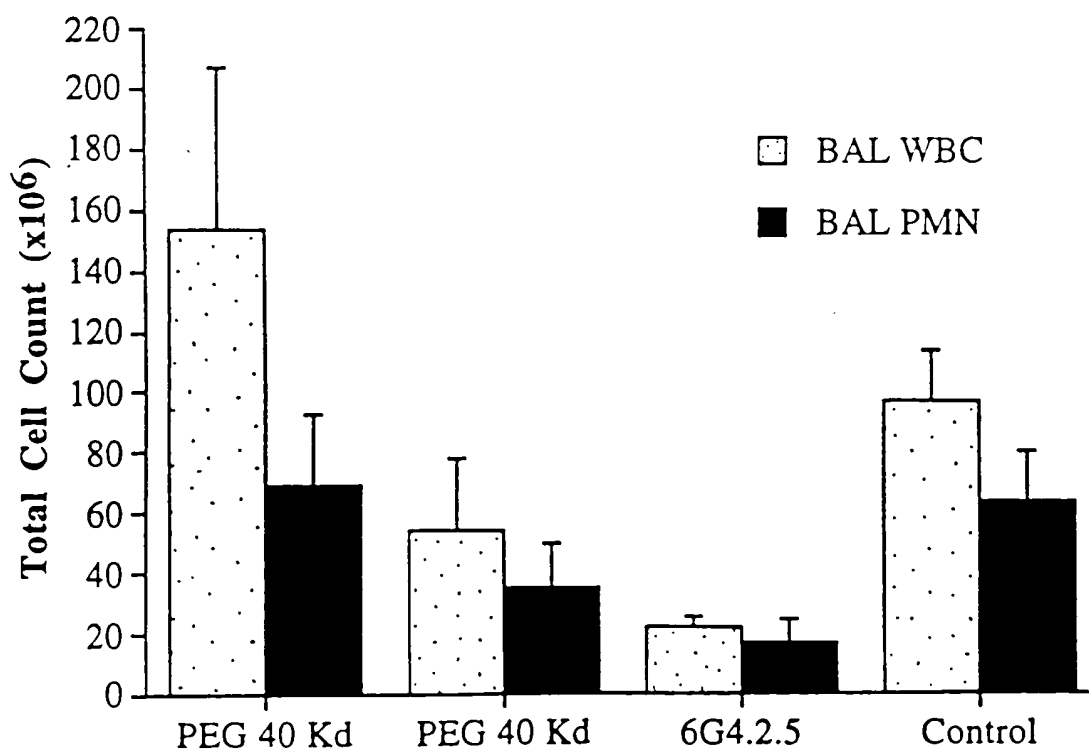


FIG. 68

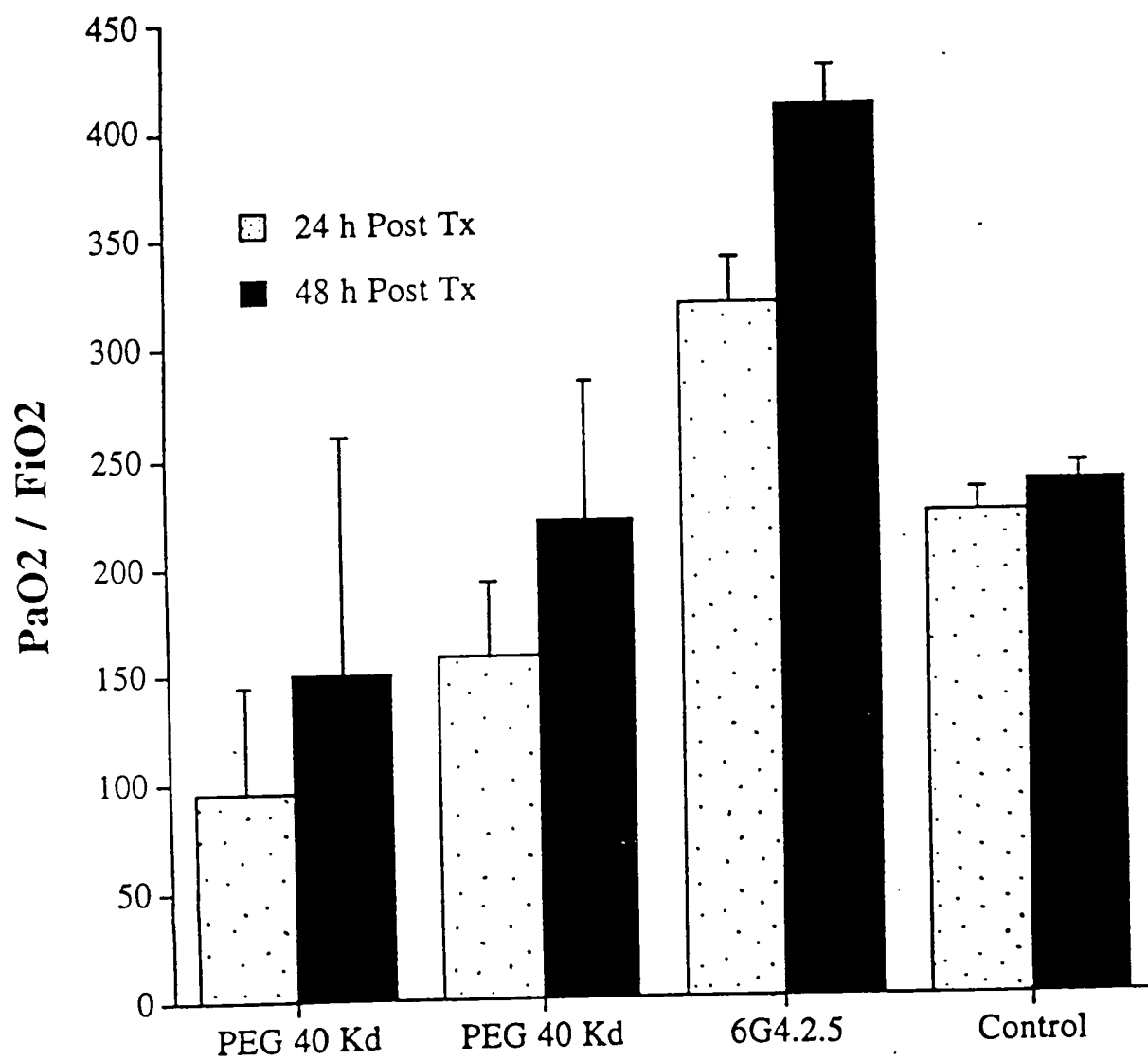


FIG. 69

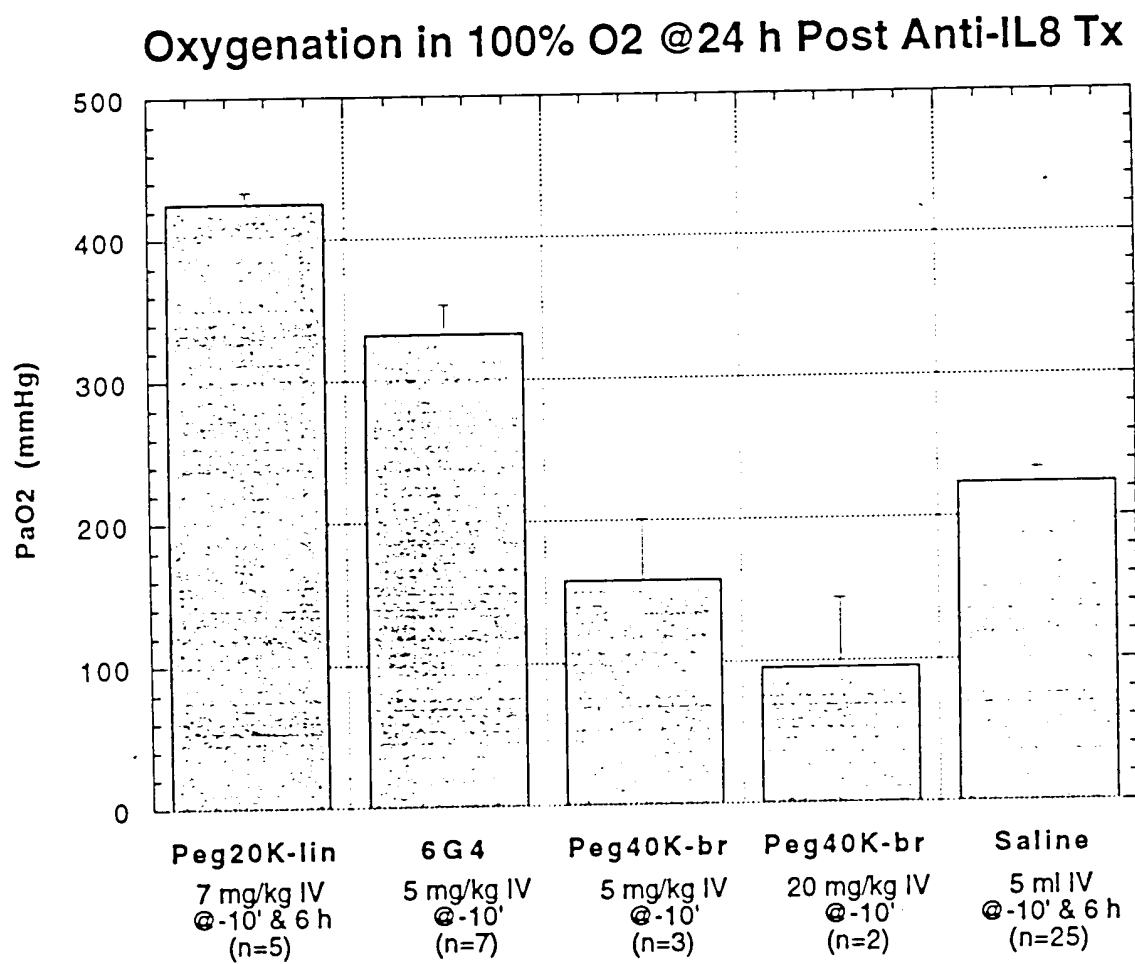


FIG. 70A

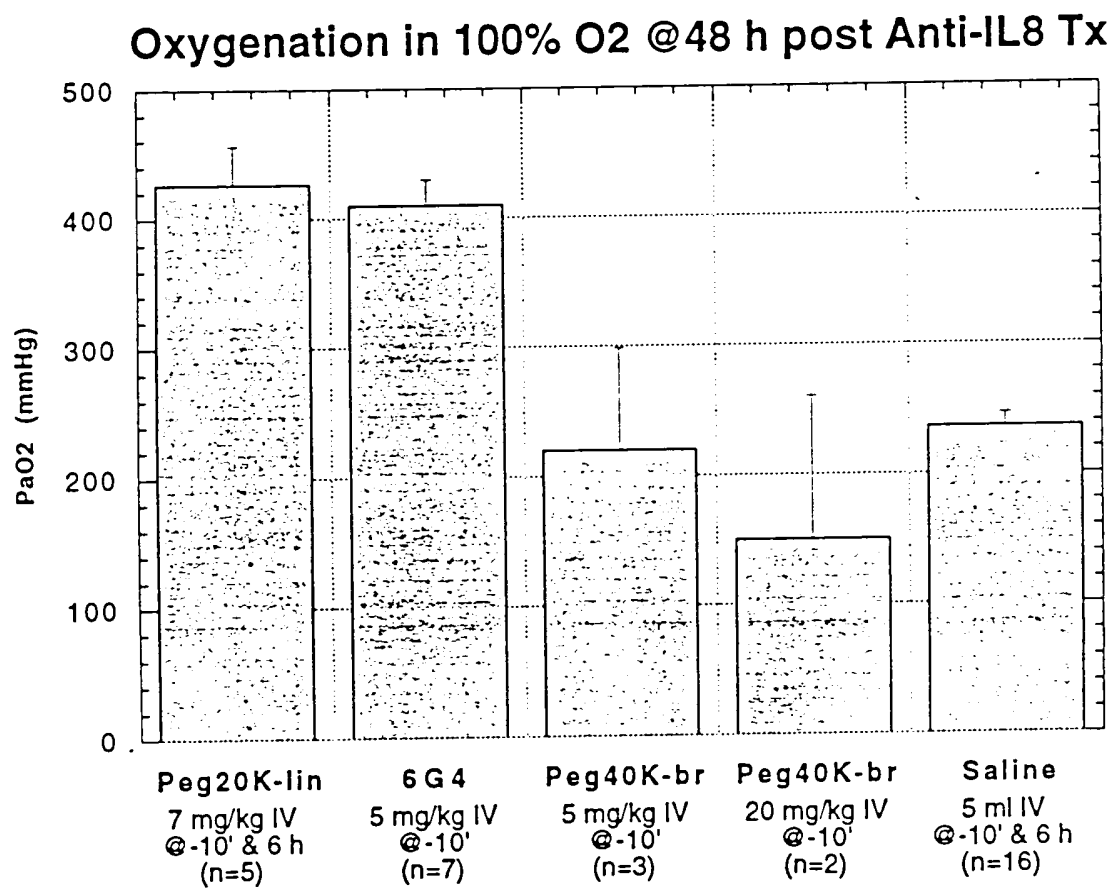


FIG. 70B

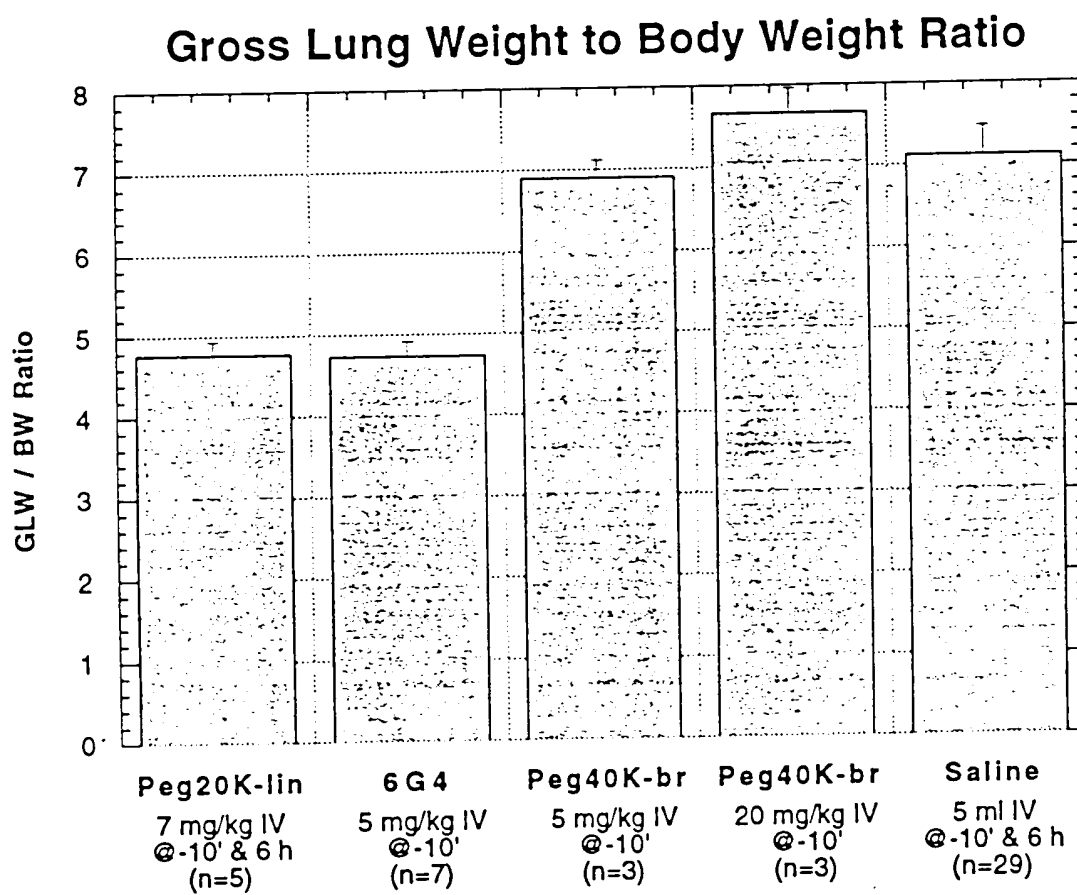


FIG. 70C

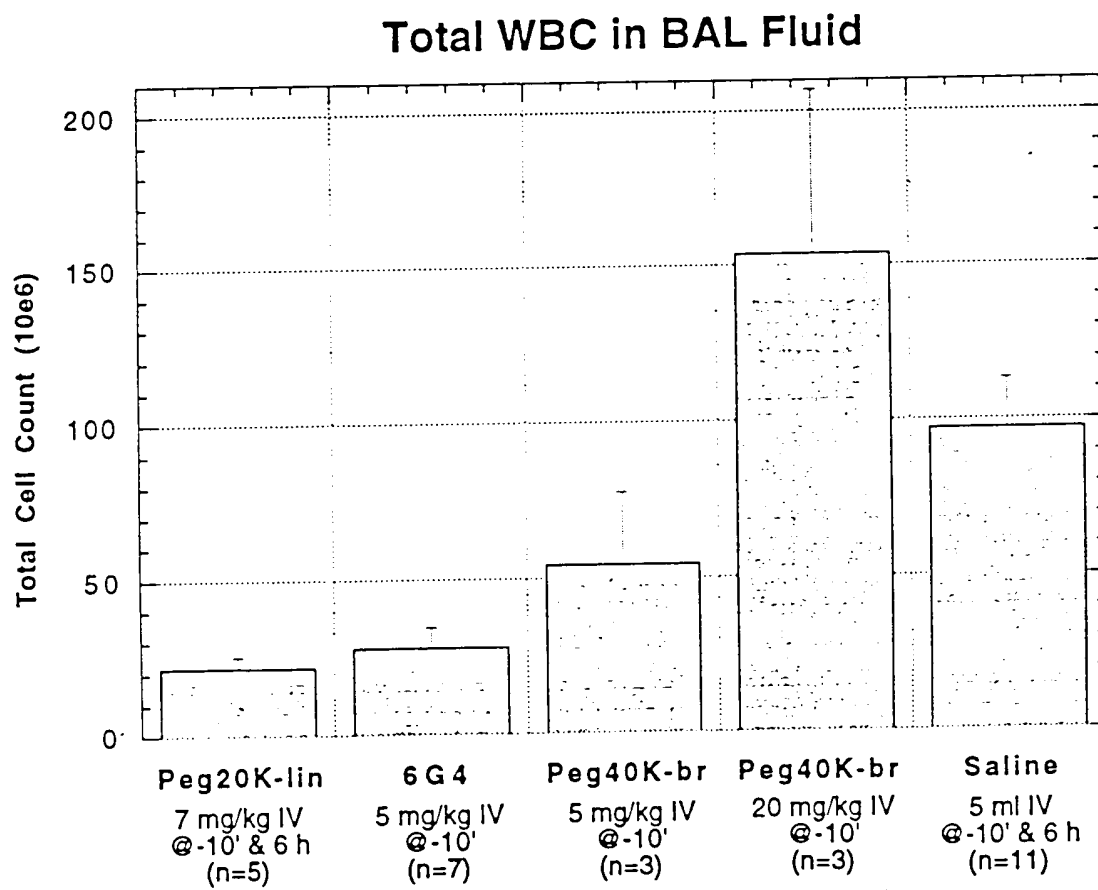


FIG. 70D

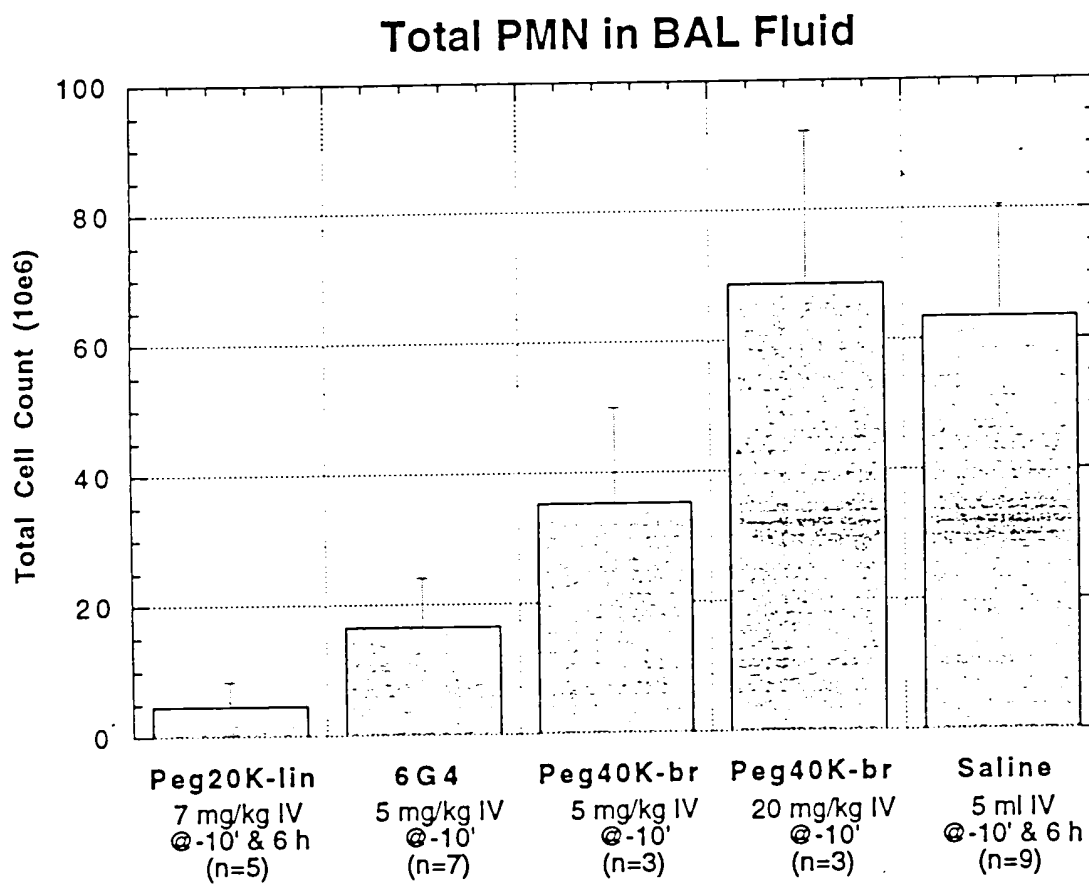
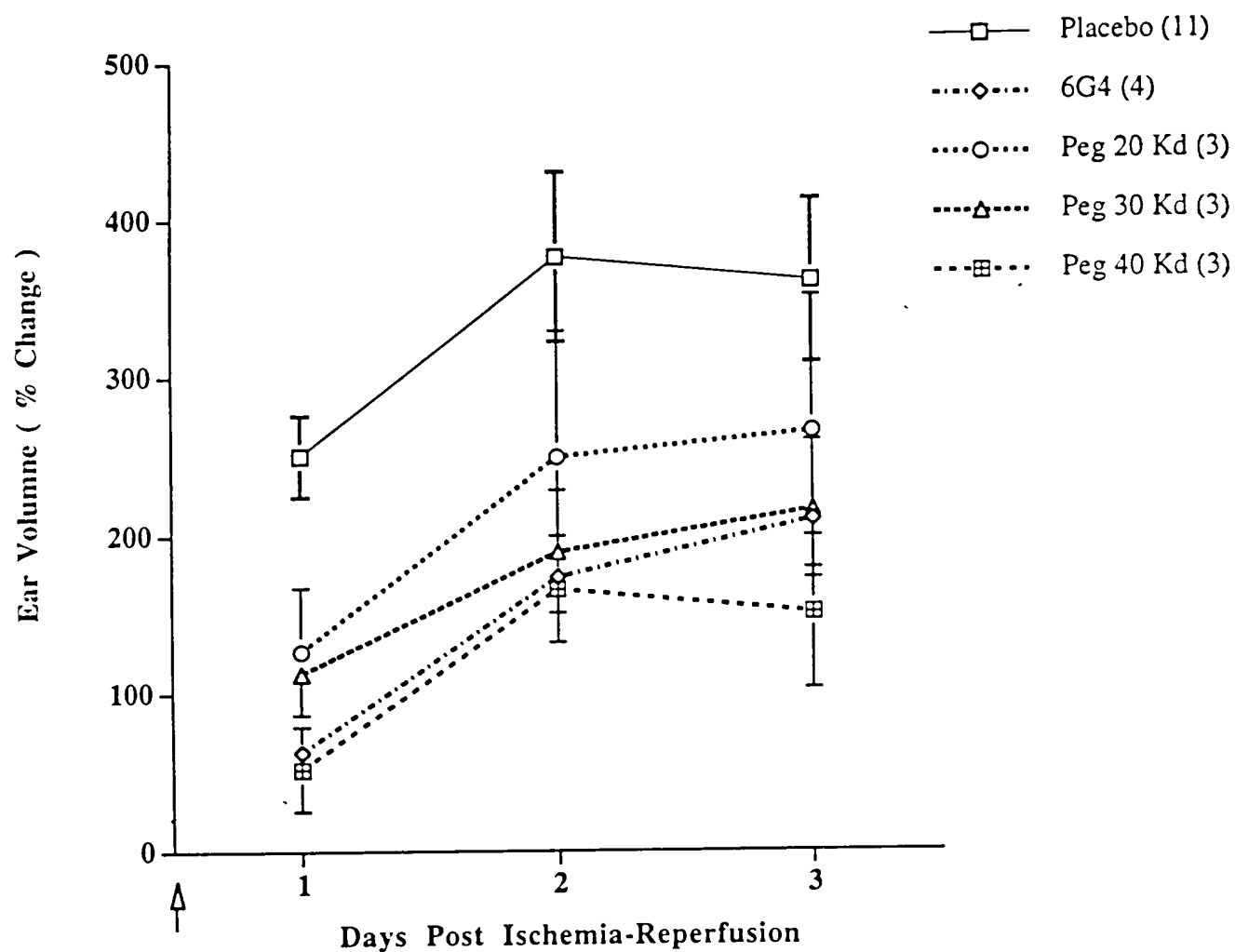


FIG. 70E

The Effect of Pegylated Anti-IL-8 in the Rabbit Ear model of Ischemia-Reperfusion Injury



Anti-IL-8 formulations :
Single Dose (5 mg/kg)
administered IV at time
of reperfusion

FIG. 71